\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* (MT)

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:48:13 1997; MasPar time 60.19 Seconds 205.147 Million cell updates/sec

Tabular output not generated.

Perfect Score: Description: Title: 28 (1-28) from US08644289.seq >US-08-644-289-3

N.A. Sequence: 1 AGTCGAATTCATTGGGACCATCCTGGCT 28

TCAGCTTAAGTAACCCTGGTAGGACCGA

Scoring table: TABLE default

Gap

Mmatch STD: Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST21 16:EST16 17:EST21 27:EST20 20:EST20 30:EST30 40:EST40 40:EST40 40:EST40 40:EST40 40:EST40 50:EST50 50:EST50 50:EST50 50:EST50 50:EST50 60:EST60 60:EST60 60:EST60 60:EST60 60:EST60 60:EST60 60:EST60 60:EST60 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74 75:EST75 76:EST76 80:EST80 80:EST80 80:EST80 80:EST80 80:EST80 90:EST90 90: EST-STS-TWO
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124
125:EST125 126:EST126 127:EST127 128:EST128 129:STS1 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 99:EST99 1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8

> Mar 25 02:47 US-08-644-289-3 rst

141:gnEST2 142:gnEST3 143:gnEST4 144:gnEST5 145:gnEST6 146:gnEST7 147:gnEST8 148:gnEST9 149:gnEST10 150:gnEST11 151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST15 152:gnEST15 157:enEST3 158:enEST2 159:enEST3 160:enEST4 161:enEST5 162:enEST6 163:enEST7 164:enEST8 173:enSTS1 174:enSTS2 165:enEST9 166:enEST10 167:enEST11 168:enEST12 169:enEST13 170:enEST14 171:enEST15 172:enEST16 136:STS8 137:STS9 138:STS10 139:ueEST 140:gnEST1 130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7

Statistics: Mean 7.030; Variance 1.506; scale 4.668

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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644-289-3 rsi

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ACCESSION DEFINITION

N51985

KEYWORDS

EST. g1193151

SOURCE

RESULT LOCUS

N51985

410 bp

ALIGNMENTS

Mar 25 02:47

US-08-644-289-3.rst

43 44 45

16 16

N50065 H93071

W18192

sclerosis 2NbHMSP vector=pT7T3D (Pharmacia) with a modified polylinker V\_TYPE: phagemid host=DH10B (ampicillin resistant) yz07f07.sl Homo sapiens cDNA clone 282373 3' similar to contains This clone is available royalty-free through LLNL; contact the Washington University School of Medicine Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; multiple sclerosis lesions from one patient was kindly provided by constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 through one round of normalization to a Cot = 5. Library RI sites of a modified pT7T vector (Pharmacia). Library went human clone=282373 primer=m13 -40 forward library=Soares multiple Alu repetitive element; contains element LTR1 repetitive element ;. Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. double-stranded cDNA was size selected, ligated to Eco RI adapters Rsitel=Not I Rsite2=Eco RI 46 year old male, 1st strand cDNA was (Pharmacia), digested with Not I and cloned into the Not I and Eco Forest Park Parkway, Box 8501, St. Louis, Consortium (info@image.llnl.gov) for further information. Pred. No. 4.01e-06; 0; Mismatchyz10h03.s1 Homo sapie yv06h04.s1 Homo sapie IMAGE: 20083 Soares in Elliston, K., Hawkins, M., 4; Length 410; EST 2 others Indels MO 63108 14-FEB-1996 <u>.</u> 2.27e-02 2.27e-02 Gaps 0 f 밁 ç 밁 DEFINITION ORIGIN FEATURES COMMENT DEFINITION RESULT ACCESSION BASE COUNT REFERENCE SOURCE KEYWORDS ACCESSION FOCUS FOCUS Query Match 64.3%; Best Local Similarity 100.0%; ORGANISM Matches AUTHORS source 186 agccaggatggtcccaat 203 187 28 AGCCAGGATGGTCCCAAT 11 27 GCCAGGATGGTCCCAATGAATTCGAC 2 gccaggatggtctcanttaattggac 212 ym97d01.rl Homo sapiens cDNA clone 166849 5' similar to contains R89652 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., vector=pBluescript SK- host=SOLR cells (kanamycin resistant) primer=-2lml3 Rsite1=EcoRI Rsite2=KhoI Placental tissue from a Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.2 kb; Uni=ZAP XR Vector; 5' adaptor sequence: 5'-GAATTCGGCACGAG-3'; 3' adaptor sequence: Alu repetitive element; contains MER22 repetitive element;  ${\tt R89652}$ Unpublished (1995) Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST  $\underline{P}roject$ Homo sapiens element. High qality sequence stops: 353 Source: IMAGE Consortium, LLNL Washington University School of Medicine Contact: Wilson RK human clone=67196 library=Stratagene placenta (#937225) T52639 ya72a11.s1 Homo sapiens cDNA clone 67196 3' T52639 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Email: est@watson.wustl.edu Fax: 314 286 1810 Tel: 314 286 1800 4444 Forest Park Parkway, Box 8501, St. Louis, WashU-Merck EST Project Eutheria; Primates; Catarrhini; Hominidae; Homo. Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; 5'-CTCGAGTTTTTTTTTTTTTTTTT-3'. g654499 18; (bases 1 to 430) 91 Conservative ø /note="human' /clone="67196" /organism="Homo sapiens" Location/Qualifiers 1..430 119 c 457 bp 430 bp Score 18; DB 115; Pred. No. 7.88e-05; 0, 104 g mRNA 353 112 t Length 430; 4 others Indels contains Alu repetitive MO 63108

ORIGIN BASE COUNT

103

ď <1..>410 /note="human"

108 c

88 g

109 t

Best Local Similarity Matches 22; Conser

67.9%; ilarity 84.6%; Conservative

Query Match

FEATURES

Location/Qualifiers

0; Gaps

0

High quality sequence stops: 188

Source: IMAGE Consortium, LLNL Email: est@watson.wustl.edu

source

/organism="Homo sapiens" /clone="282373"

COMMENT

TITLE

Wilson, R.

JOURNAL

Unpublished

The WashU-Merck EST Project Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T.,

(bases 1 to 410)

ORGANISM

Homo sapiens

Dr. Kevin G. Becker (NINDS/NIH).

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08-FEB-1995

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REFERENCE
AUTHORS
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Best Local Similarity 87.5%;
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                            172 gaatgcagtggcaccatcctggct 195
  5 GAATTCATTGGGACCATCCTGGCT 28
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
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WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human clone=166849 library=Soares adult brain N2b4HB55Y vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsitel=Not I Rsite2=Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stops: 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
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/clone="166849"
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Pred. No. 7.88e-05;
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                                                                                                                                                              Length 457;
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Locus Mar 25 02:47 SOURCE KEYWORDS ACCESSION DEFINITION g1080914 н90484 Alu repetitive element; . yv01g06.rl Homo sapiens cDNA clone 241498 5' similar to contains H90484 host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver cDNA was primed with a Pac I - oligo(dT) primer [5' and spleen from a 20 week-post conception male fetus. 1st strand human clone=241498 primer=M13RP1 library=Soares fetal liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker 473 bp US-08-644-289-3.rst 28-NOV-1995

ORGANISM I and cloned into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

REFERENCE Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 473)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Unpublished (1995) The WashU-Merck EST Project ∦ilson,R.

COMMENT JOURNAL

WashU-Merck EST Project Contact: Wilson RK

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine

High quality sequence stops: 371 Source: IMAGE Consortium, LLNL Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the [MAGE Consortium (info@image.llnl.gov) for further

FEATURES source 1..473 Location/Qualifiers

131 a <1..>473 a 74 c /note="human" /clone="241498" /organism="Homo sapiens" 113 g 152 t

3 others

ORIGIN BASE COUNT

Matches Query Match 64.3%; Best Local Similarity 87.5%; 21; Conservative Score 18; DB 34; Pred. No. 7.88e-05; <u>.</u>. Mismatches Length 473; Indels 0; Gaps

0;

င့ 28 94 agccaggatggtgccactgcattc 117 AGCCAGGATGGTCCCAATGAATTC 5

RESULT ACCESSION DEFINITION yp69b12.rl Homo sapiens cDNA clone 192671 5' similar to contains Alu repetitive element; contains THR repetitive element;.

RESULT

US-08-644-289-3.rst

Mar 25 02:47

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RESULT
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Best Local Similarity 87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holman, M., Hultman, M., Kucaba, T., Le, M., Lenno, Parsons, J., Rifkin, L., Rohlfing, T., Soares, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Clark, N., Dubuque, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 midbrain, pons and medulla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subcortical white matter, basal ganglia, thalamus, cerebellum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aortic aneurysm. RNA was prepared from a pool of tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RI sites of a modified pT/T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human clone=192671 library=Soares adult brain N2b4HB55Y vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI
  T99302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed by Bento Soares and M.Fatima Bonaldo. The adult brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stops: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was size selected, ligated to Eco RI adapters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55-year old male.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Pharmacia), digested with Not I and cloned into the Not I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 509)
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                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/clone="192671"
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                                                                                                                                                                                                                         Pred. No. 7.88e-05;
                                                                                                                                                                                                                                               Score 18,
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                                                                                                                                                                                                                                                                                            Best Local Similarity 83.3%;
Matches 20; Conservation
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                                                                                                                                                                                                                                         114 tcgcattntttgggactatcctgg 137
                                                                                                                                                                                                                 3 TCGAATTCATTGGGACCATCCTGG 26
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                                                                                           All38R Homo sapiens cDNA clone All38 similar to Alu repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High qality sequence stops: 1
Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g749039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High qality sequence starts: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by Bento Soares and M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I and cloned into the Pac I and Eco RI sites of the modified pT7T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liver and spleen from a 20 week-post conception male fetus. 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI
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Pred. No. 1.41e-03;
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ye76d09.s1 Homo sapiens cDNA clone 123665 R02746
                                                                                                                                                                                                                                                                 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p7773 vector. Library went through one round of normalization. Library
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Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Unpublished (1995)
                                                               Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                         Holman, M., Hultman, M., Kucaba, T.,
                                                                                                                                  Hillier, L.,
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                       Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo (dT) primer (5')
                                                                                                                                                                                                                                                                                                                                                                                                                                                     human clone=123665 library=Soares fetal liver spleen 1NFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. USA 91, 10645-10649 (1994)
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                       The WashU-Merck EST Project
                                                                                                                                                                               Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                    Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                                              constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                              vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
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                                                                                                             Le, M., Lennon, G., Marra, M.,
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Best Local Similarity 84.0%;
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                                                                                                             Key
                                                                                                                                                            est@watson.wustl.edu High quality sequence stops: 340 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL
                                                                                                                                                                                             School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
                                                                                                                                                                                                                               Contact: Wilson RK WashU-Merck EST Project Washington University
                                                                                                                                                                                                                                              Unpublished.
                                                                                                                                                                                                                                                                                              Holman M., Hultman M., Kucaba T., Le M., Lennon G., Ma
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
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                                                                                                                           contact the IMAGE Consortium (info@image.llnl.gov) for further nformation. NCBI gi: 1225181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; RNA; EST; 443
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Best Local Similarity 100.0%;

Score 17; DB 157; Pred. No. 1.41e-03;

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Best Local Similarity 100.0%;
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WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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zbl4f11.sl Homo sapiens cDNA clone 302061 3'.
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zb03c03.sl Homo sapiens cDNA clone 300964 3'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
                                Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson
"The WashU-Merck EST Project";
                                                                 Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
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Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra
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Contact: Wilson RK WashU-Merck EST Project Washington University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            information. NCBI gi: 1243382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="300964"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 164;
Pred. No. 2.27e-02;
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                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                 Marra M.,
                                                                                                                                               Hominidae
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Best Local Similarity 86.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     information. NCBI gi: 1242312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; contact the IMAGE Consortium (info@image.llnl.gov) for further
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 CCAGGATGGTCCCAATGAATTC 5
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                                                                                                                                   Cloning method: total mRNA was oligo-(dT) primed and directionally cloned \bar{5}' -> 3' into the HindIII -> NotI sites of the lafmid BA
                                                                                                                                                                                  C.R. Acad. Sci., III, Sci. Vie 318, 263-272 (1995)
                                                                                                                                                                                                                                                   Auffray, C., Behar, G., Bois, F., Boucher, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. sapiens partial cDNA sequence;
                                           cDNA sequence complementary to mRNA (3'end)
                                                                  Primer: (-21)M13_universal;
                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19~JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        partial cDNA sequence; transcribed sequence fragment.
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  Normalization method: Bento Soares, P.N.A.S in
                       Stretch_removed:
                                                                                        Sequencing_method: single read,
                                                                                                                                                                                                                                IMAGE: Integated molecular analysis of the human genome and its
                                                                                                                                                                                                                                                                                                                                                                                             The Genexpress cDNA program
                                                                                                                                                                                                                                                                                                                                                                                                                     Genexpress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genethon, B.P. 60, 91002 Evry Cedex France and Genetique
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
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                       removed at sequence 5'end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>.
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                                                                                          full automatic;
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   Matches
                 Query Match 57.1%;
Best Local Similarity 94.4%;
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Best Local Similarity 94.4%;
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hbc022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                   Univ. of Chicago
                                                                                                                                                                                                                                                                                                                                                                                             A molecular inventory of human pancreatic islets:sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                  Bell, G.I. and Takeda, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human clone-hbc022 library=Human pancreatic islet vector=Lambda ZAPII primer=SK primer Rsitel=Eco RI Rsite2=Xho I mRNA was prepared from normal adult human islets. cDNA was directionally synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g390714
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                                                                                                                                                                                                          Email: g-bell@uchicago.edu.
                                                                                                                                                                                                                                             5841 S. Maryland Ave., MC1028, Chicago IL 60637
Tel: 3127029116
                                                                                                                                                                                                                                                                                                                      Contact: Bell GI or Takeda J
                                                                                                                                                                                                                                                                                                                                                             Hum. Mol.
                                                                                                                                                                                                                                                                                                                                                                               of 1000 cDNA clones
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                                                                                                                                                                                                                             Fax: 3127020271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from the Xho I in the vector to the EcoRI site. cDNA was size fractionated to remove sequences <1000 bp in size.
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                                                                                                              /note="Human"
                                                                                                                                                                      Location/Qualifiers
1..252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="normalized infant brain cDNA from B.Soares, Psychiatry Dept. Columbia University USA"
                                                                                                                                /organism="Homo sapiens"
/clone="hbc022"
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56 c 43 g 67 t
                                                                                                                                                                                                                                                                                                                                                           Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="female"
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Pred. No. 2.27e-02;
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Pred. No. 2.27e-02;
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                                                                              Query Match 57.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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15
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Human STS UT854, 5' primer bind
L31251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer A: Primer B:
                                                                                                                                                                                                                                                                                                                                                         Cycles Denaturation Annealing Extension C 10 sec. 62 C 10 sec. 72 C 20 sec. 31 Sec. 72 C 20 sec. 31 Sec. 72 C 20 sec. Mg++: 1.25 mM Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence tagged sites from the human genome Unpublished (1994) See COMMENT for author address
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 284)
Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted by: Utah Center for Human Genome Research University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                           Alleles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           End to Label: Primer B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial Denaturation: 94C 300sec
                                                                                                                                                                                          93 a
                                                                                                                                                                                                                                   /sequenced_mol="DNA"
4..22
                                                                                                                                                                                      /evidence=experimental
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTACAGGTGTAAGCCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGTCAGGAGATTGAGACC
                                                                              Score 16; DB 138; Length 284; Pred. No. 2.27e-02; 0; Mismatches 1; Indels
                                                                                                                                                                                          43 t
                                                                                  1; Indels 0;
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                                                                                                                                                                                          10 others
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                                                                                                                                                                                                                                                                                                                                                                                                      94 C
                                                                                  Gaps
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10 sec.
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Search completed: Tue Mar 25 02:49:22 1997 Job time : 69 secs.

Mar 25 02:41 US-08-644-289-2.rng

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:42:30 1997; MasPar time 10.59 Seconds 312.999 Million cell updates/sec

Tabular output not generated.

Title: >US-08-644-289-2 (1-38) from US08644289.seq 38

Description: Perfect Score:

N.A. Sequence: 1 AGTCAGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38 TCAGTCCGGAATCTCAATTTCCTACGGGTACGATGTCT

Scoring table: TABLE default Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.939; Variance 3.336; scale 1.780

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

8 7	<b>6</b> 5	c 4-3	2	-	Result No.	
19 19	19 19	26 24	34	38	Score	
50.0	50.0 50.0	68.4 63.2	89.5	100.0	Query Match	ωļo
1062 1181	471 984			38	Query Match Length DB	
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Q62359 Q97854	_Q62363 Q62361	Q51746 Q51746	Q67883	T10486	ID	COLHERA
Fragment coding for h Human p53 cDNA.	Fragment coding for h Fragment coding for h	Oligonucleotide probe Oligonucleotide probe	Murine p53 DNA.	Human wild-type p53 q	Description	
2.07e-01 2.07e-01	2.07e-01 2.07e-01	1.47e-05 2.46e-04			Pred. No.	

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Plasmid pBRV2 insert Sequence encoding hum Plasmid pBRG4 insert Streptomyces nodosus Sequence of human gra Tobacco mosaic virus Protease gene.	myoD retroviral expre MoMIV gag/pol gene re MoMIV gag/pol gene re Wector M48 used for g myoD retroviral expre pXJCL-hGM-CSF express Babesia sp. oligonucl	Wild type p53 gene se Sequence encoding 53 Human p53 DNA. Vaccinia H6 promoter/ Vaccinia H6 promoter/ Vaccinia H6 promoter/ Mutant p53 polypeptid Mixed oligonucleotide Base substituted E.co MoMLV gag matrix prot MoMLV mutated gag mat MoMLV mutated gag mat MoMLV gag/pol gene pr Human Natriuretic Pep Hybrid vector pSF3. Hybrid vector pSF2. Hybrid vector pSF1. Hybrid vector pSF1. Hybrid vector pSF1. Hybrid vector pSF3. Hybrid vector pSF1. Hybrid vector pSF3. Hybrid vector pSF1. Hybrid vector pSF1. Hybrid vector pSF3. Hybrid vector pSF1. Hybrid vector pSF1. Hybrid vector pSF1. Hybrid vector pSF3. Hybrid vector pSF3. Hybrid vector pSF1. Hybrid vector pSF3.	US-08-644-289-2.mg
2.94e+01 2.94e+01 2.94e+01 2.94e+01 2.94e+01 2.94e+01 2.94e+01 2.94e+01 2.94e+01 2.94e+01	8. 93e+00 8. 93e+00 8. 93e+00 8. 93e+00 8. 93e+00 8. 93e+00 8. 93e+00 2. 94e+01	2.07a-01 2.07a-01 2.07a-01 2.07a-01 2.07a-01 2.07a-01 2.07a-01 2.07a-01 2.07a-01 2.02a+00 8.93a+00	

## ALI GNMENTS

င္ပ	ន	CC	PS	PT	ΡŢ	PΤ	DR	ΡI	PΑ	PR	ЭF	PD	PN	SO	¥	Ş	Ş	DE	DT	AC	ID	RESULT
gene. An epitope from intron 10 of the human p53 gene is used to	N-terminal (nucleotides -111 to 1090) portion of the wild-type p53	T10486-T10488 are primers used in a RT-PCR reaction to obtain an	Disclosure; Page 7; 40pp; English.	individual treatment regimes.	useful in diagnosis or prognosis of cancer, and for establishing	New antibodies specific for alternatively spliced mammalian p53 -	WPI; 96-140137/15.	Kulesz-Martin MF;	(HEAL-) HEALTH RES INC.	14-JUN-1994; US-259612.	05-JUN-1995; 150994.	15-DEC-1995.	CA2150994-A.	Homo sapiens.	reverse transcriptase polymerase chain reaction; ss.	proliferative disorder; psoriasis; prognosis; diagnosis; cell cycle;	Tumour suppressor; p53; alternative splicing; antibody; cancer;	Human wild-type p53 gene N-terminal sense RT-PCR primer.	03-OCT-1996 (first entry)	T10486;	T10486 standard; DNA; 38 BP.	LIT 1

w

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CC as a template. The 228 bp amplified fragment contains the H6 promoter CC and the 5'-most bases of the murine p53 gene. Fragment II was produced CC using primers MM082 and MM083 and plasmid p11-4 as a template. The 129 CC bp amplified fragment contains the 3' end of the H6 promoter, the 5'-most CC bases of the murine p53 gene, and 15 bp which overlap fragment III. CF fragment III was produced using primers MM084 and MM085 and plasmid CC p11-4 as a template. The 301 bp amplified fragment contains the 3' end CC of the p53 gene, and the 5' end overlaps fragment II. The three PCR CC products were pooled and primed with MM080 and MM085. The resultant 588 CC inserted into pNC5LSP5 to generate plasmid pMM148 containing H6 promoted CC inserted into pNC5LSP5 to generate plasmid pMM148 containing H6 promoted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  murine; interleukin-2; II-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector; plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response; polymerase chain reaction; poxvirus; pSD542; immunological response;
                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the wildtype murine p53 gene from the translation initiation codon to the stop codon. This sequence was used in the construction of an ALVAC-based recombinant virus containing the wild-type murine p53 gene. Three PCR fragments were generated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JT 2
Q67883 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spliced p53. The antibodies are useful in the diagnosis and prognosis of human cancer and in the study of p53 and alternatively spliced p53
                                                          C5 locus.
                                                                                                       between
                                                                                                                        wildtype murine p53 in the ALVAC C5 insertion locus. Recombination
                                                                                                                                                                                                                                                                                                                                                                         Fragment I was produced using primers MM080 and MM081 and plasmid pRW825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding cytokine and/or tumour associated antigen Example 31; Fig 38; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q67883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells they may cause cell cycle arrest. Vectors contg. p53as cDNA may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     create antibodies directed against this sequence in an alternatively
                                      an antigenic or immunological response, ie. for immunisation
                                                                               virus vCP263, which contains the vaccinia H6 promoted murine p53 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 94-263767/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cox WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1994; U00888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogen; human; interferon; IFN; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be used in gene therapy of cancers and other proliferative
                       pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Attenuated recombinant virus used for cancer therapy - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9416716-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine p53 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (p53as) and their expression. When the antibodies are injected into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                   this donor plasmid and ALVAC rescuing virus produced recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paoletti E, Tartaglia J;
 1173 BP;
                                                            The resulting virus may be used in a composition for inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 A;
 279 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.73e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 C;
349 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
304 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                        against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q51746 standard;
Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1028 aggccttagagttagaggatgcccatgctacaga 1061
  Oligonucleotide probe
                      Claim 3; Page 14; 23pp; English.
                                                  samples
                                                                                                                                                             Shank DD,
                                                                                                                                                                                                                   24-MAY-1993; 108325.
26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                        01-DEC-1993.
                                                                                                                                                                                                                                                                                                  EP-571911-A.
                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q51746 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be useful as an initial screen for mycobacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 93-378844/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1994
                                                                            detection and amplification of Mycobacteria nucleic acid
                                                                                                        New oligo:nucleotide probes specific for Mycobacteria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   samples
                                                                                                                                                                                         (BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BECT ) BECTON DICKINSON CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGTCAGGCCTTAGAGTTAAAGGATGCCCATGCTACA
                                                                                                                                    93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                           Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spears PA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA;
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0.0%;
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MK14-A consists of nucleotides 5-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
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Pred. No. 1.47e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Mismatches
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RESULT
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Matches 24; Conser
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Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
               062361;
                            JT 6
Q62361 standard; cDNA; 984
                                                                                                                                                                                                                                                                                                                                   Non-radioactive detection of p53 specific antibodies — on immobilised p53 or its fragments, then reaction with second antibody, for diagnosis of tumours and suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 5
Q62363 standard;
                                                                                                                                                                                                    each of these fragments.
Sequence 471 BP; 128 A;
                                                                                                                                                                                                                                                                                                                                                                                               Klein R, Schranz P,
WPI; 94-135732/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contain start or stop codons"
 18-NOV-1994
                                                                                                                                                                                                                                                             region. Preferred fragments contain amino acids 1-241, 40-349,
                                                                                                                                                                                                                                                                            fragments of the p53 gene product containing the antibody-binding
                                                                                                                                                                                                                                                                                       Antibodies specific for p53 are detected by binding to immobilised
                                                                                                                                                                                                                                                                                                        Claim 13; Page 25; 35pp; German.
                                                                                                                                                                                                                                                                                                                        screening
                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; R51878.
                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1993; E02666.
30-SEP-1992; DE-232823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transl_except=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= p53(237-393)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-oncogene; cancer; tumour; antibody binding region; epitope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human nuclear phosphoprotein p53; tumour suppressor gene product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fragment coding
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                                                                                                                                                                                                                                    368-386.
                                                                                                                                                                                                                                                                                                                                                                                                                            (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 TCTGTAGCATGGGCATCCTTTAACTCTAAGGCCT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 hhvvhhvhvsvvvvhhvvhhvhvhyhvyvsvct 62
                                                                                       AGGCCTTAGAGTTAAAGGATGCCCATGCT 33
                                                                                                  aggeettggaacteaaggatgeecagget 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 partial CDS, therefore sequence
                                                                                                                                                                                                                                 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or . See Q62357-Q62366 for nucleic acid sequences coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for human p53 amino acids 237-393.
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                                                                                                                                                          50.0%;
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Pred. No. 2.46e-04;
27; Mismatches 5
                                                                                                                                                           Pred. No. 2.07e-01
                                                                                                                                                                          Score 19;
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                                                                                                                                                                                                    133 C;
                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Volkmann M,
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> Mar 25 02:41 US-08-644-289-2.mg

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Ş 밁 Matches Query Match 50.0%; Best Local Similarity 82.8%; Antibodies specific for p53 are detected by binding to immobilised fragments of the p53 gene product containing the antibody-binding region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or 368-386. See Q62357-Q62366 for nucleic acid sequences coding for 30-SEP-1993; E02666.
30-SEP-1992; DE-232823.
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.
Klein R, Schranz P, Tessmer C, Volkmann M, each of these fragments.
Semmence 984 BP; 224 A; Klein R, Schranz WPI; 94-135732/16. WO9408241-A. Homo sapiens. Human nuclear Q62359 standard; Claim 13; Page 24; 35pp; German. screening second antibody, for diagnosis of tumours and suitable for on immobilised p53 or its fragments, then reaction with labelled Non-radioactive detection of p53 specific antibodies - by capture WPI; 94-135732/16. Klein R, W09408241-A. contain start or stop codons' /transl\_except= pos:622..624,aa:Arg
/note= "partial CDS, therefore sequence does not Homo sapiens. Human nuclear phosphoprotein p53; tumour suppressor gene product; contain start or stop codons" /transl\_except= pos:700..702,aa:Arg
/note= \*\*partial CDS, therefore sequence anti-oncogene; Fragment coding for human p53 amino acids 40-393. P-PSDB; R51876. (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG. 30-SEP-1992; 30-SEP-1993; anti-oncogene; cancer; tumour; antibody binding region; epitope; ds Fragment coding for human p53 amino acids 66-393. 14-APR-1994. /product= p53(40-393) 18-NOV-1994 (first entry) 14-APR-1994. /product= p53(66-393) 842 aggccttggaactcaaggatgcccaggct 870 5 AGGCCTTAGAGTTAAAGGATGCCCATGCT 24; Schranz P, Tessmer C, Conservative DE-232823. phosphoprotein p53; tumour suppressor gene product; cancer; tumour; antibody binding region; epitope; Location/Qualifiers 1..1062 cDNA; Location/Qualifiers 1062 В₽ Score 19; DB 11; Pred. No. 2.07e-01; 0; 311 C; Mismatches Volkmann M, does not 259 G; 5 Length 984; Zentgraf Zentgraf 190 Ξ Æ 0 Gaps ds. 0;

by capture labelled

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Best Local Similarity 82.8%;
Matches 24; Conservative
                                                              Matches
                                                                         Query Match 50.0%;
Best Local Similarity 82.8%;
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23-MAY-1994; US-247904.
27-MAY-1994; US-250795.
13-SEP-1994; US-305520.
                              1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q97854;
                                                                                                                                                Disclosure; Page 105-106; 157pp; English.

Human p53 cDNA (given in Q97854) was amplified from a HeLa cell cDNA library using the primers given in Q97852-53. The gene was subcloned into a baculovirus vector for expression of recombinant p53 in Sf9 insect cells for use as a component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ubiquitin-conjugating enzyme; p53 protein; cell cycle; cell proliferation; cancer; psoriasis; fibrosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .T 8
Q97854 standard; cDNA; 1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or 368-386. See Q62357-Q62366 for nucleic acid sequences coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 22; 35pp; German.
                                                                                                                     an in vitro ubiquitin conjugating system. Sequence 1181 BP; 275 A; 366 C;
                                                                                                                                                                                                                              e.g. cell proliferation
                                                                                                                                                                                                                                                           regulatory proteins - also new ubiquitin conjugating enzymes, their
                                                                                                                                                                                                                                                                                              P-PSDB; R79658.
                                                                                                                                                                                                                                                                                                           WPI; 95-255137/33.
                                                                                                                                                                                                                                                                                                                          Cottarel G,
                                                                                                                                                                                                                                                                                                                                          (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     04-JAN-1995; U00164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09518974-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human p53 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               each of these fragments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        screening
                                                                                                                                                                                                                                           related nucleic acid, vectors, antibodies etc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                           dentifying inhibitors of ubiquitin mediated proteolysis of cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       920 aggccttggaactcaaggatgcccaggct 948
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AGGCCTTAGAGTTAAAGGATGCCCATGCT 33
              aggccttggaactcaaggatgcccaggct 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1062 BP;
                                                                                                                                                                                                                                                                                                                          Draetta G,
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 A;
                                                                                                                                                                                                                                                                                                                          Eckstein JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19;
Pred. No.
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                                                                         Score 19; DB 15;
Pred. No. 2.07e-01;
                                                           0
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                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                          Gyuris J,
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                                                                                                                      306 G;
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                                                           5.
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                                                                                         Length 1181;
                                                                                                                                                                                                                                              useful for regulating
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                                                            Indels
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                                                                                                                        234 T;
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                                                           Gaps
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Mar 25 02.41 US-08-644-289-2.mg

Ş 밁 Query Match Best Local S Matches Use of wild-type p53 gene - in a medicament for suppressing the neoplastic phenotype of a cancer cell lacking wild-type p53 protein Claim 1; Page 5; 25pp; English.

The wild-type p53 gene can be used in the production of a medicament for suppressing the neoplastic phenotype of a cancer cell lacking T29719; 50.0%; t Local Similarity 82.8%; l ches 24; Conservative or prostate carcinoma cells. endogenous ward type per percent cells, lung carcinoma cells, lymphoma fashion include osteosarcoma cells, lung carcinoma cells or breast, bladder endogenous wild type p53 protein. Cancer cells suppressed in such WPI; 96-223439/23. Chen P, /product= p53 protein. misc\_difference 19..21 /\*tag= Homo sapiens. osteosarcoma cells; lung carcinoma cells; lymphoma cells; p53 gene; Wild type p53 gene sequence. 29-OCT-1996 (first entry) T29719 standard; cDNA; 1182 P-PSDB; R91933. 24-AUG-1990; 08-MAY-1996. bladder cells; prostate carcinoma cell; ss. (REGC ) UNIV CALIFORNIA. 23-AUG-1991; /transl\_except= CAT encodes /\*tag= leukaemia cells; soft tissue sarcoma cells; breast cells; 9 Lee W; cancer; carcinoma; neoplastic; neoplasia; 1182 BP; US-573405. 307791. 1..1182 Location/Qualifiers 278 A; Score 19; DB 22; Pred. No. 2.07e-01 Aspartic Β₽ 0; Mismatches 366 C; acid. 304 G; 5; Length 1182; Indels phenotype; 234 T; <u>,</u> Gaps ç

Q22995 standard; DNA; 1182 BP

23-AUG-1991; 307791.
24-AUG-1990; US-573405.
(REGC ) UNIV OF CALIFORNIA.
Lee WH, Chen PL;
WPI; 92-090221/12. 23-JUI-1992 (first entry)
Sequence encoding 53 kD cellular protein.
Cancer therapy; cancer suppressor gene; c EP-475623-A. Homo sapiens. 18-MAR-1992. /\*tag= Location/Qualifiers gene; oncogenesis;

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5 AGGCCTTAGAGTTAAAGGATGCCCATGCT 33

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Best Local Similarity 82.8%;
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1037 aggccttggaactcaaggatgcccaggct 1065
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                                                                                                                                                                                                        virus produced recombinant virus vCP270, which contains the vaccinia H6 promoted mutated human p53 in the C5 locus. The resulting virus may be
                                                                                                                                                                                                                                               The plasmid pMM110 (see also Q67864) contains the vaccinia H6 promoter and the wild type human p53 gene in the ALVAC C5 insertion site. The mutant p53 gene was obtained from plasmid Cx22A and cloned into pMM110 to generate pMM143. Recombination between pMM143 and ALVAC rescuing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; murine; interleukin-2; II-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response; polymerase chain reaction; poxyirus; pSD542; immunological response; polymerase chain reaction; poxyirus; pSD542; immunological response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1182 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colon carcinoma, lymphoma, leukaemia, etc., suggesting that mutation of the p53 genes is involved in oncogenesis. Specifically 273 Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes. Variant forms of p53 are found in human breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53 cDNA, or its gene prods., can be used to suppress and eradicate
cancers caused by defective, mutant or absent cancer suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,T 11
Q67884 standard; DNA; 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is replaced by 273 His, a mutation found exclusively in tumour cells. Sequence 1182 BP; 277 A; 368 C; 303 G; 234 T;
                                                                                                                                                                                     used in a composition for inducing an antigenic or immunological
                                                                                                                                                                                                                                                                                                                                 position 524, changing an Arg residue at position 175 to a His residue
                                                                                                                                                                                                                                                                                                                                                                              construction of an ALVAC-based recombinant virus containing a mutant
                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the wildtype human p53 gene from the translation
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 32; Fig 39; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding cytokine and/or tumour associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 94-263767/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VIRO-) VIROGENETICS CORP.
Cox WI, Paoletti E, Tartaglia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-1994; U00888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09416716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen; human; interteron; IFN; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human p53 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q67884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 15; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neoplastic phenotype e.g. in osteo-sarcuma(s), leukaemia(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloned p53 cDNA and protein prods. - for suppression of
                                                                                                                                                                                                                                                                                                                                                        form of the human p53 gene. The mutant form has a G>A substitution at
                                                                                                                                                                                                                                                                                                                                                                                                 initiation codon to the stop codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Attenuated recombinant virus used for cancer therapy - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ymphoma(s), etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 50.0%;
Local Similarity 82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AGGCCTTAGAGTTAAAGGATGCCCATGCT 33
                                                                                                                                                1182 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                              Conservative
                                                                                                                                                                 for immunisation against pathogens.
                                                                                                                                              276 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 19; DB 3; Le
; Pred. No. 2.07e-01;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Β₽
                                                                             Score 19; DB 12;
Pred. No. 2.07e-01

 Mismatches

                                                                                                                                              365 C;
                                                                                                                                                                                                                                                                                                                                                                                             This sequence was used in the
                                                                                                                                              307 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1182;
                                                              5
                                                                                                     Length 1182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                              Indels
                                                                                                                                              234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lung or
                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TK vector;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                              0
```

Ş Matches Query Match 50.0%; Best Local Similarity 82.8%; 1269 aggccttggaactcaaggatgcccaggct 1297 Q67864; viruses, and into NYVAC to give vP1101, vP1096 and vP1098. The viruses may be used in a composition for inducing an antigenic immunological response, ie. for immunisation against pathogens. Sequence 1483 BP; 367 A; 415 C; 372 G; 329 T; Q67864 standard; plasmid, ALVAC, to give vCP207, vCP193 and vCP191 recombinant gene. The expression cassettes generated by linking the vaccinia H6 promoter and the p53 genes may be cloned in to the poxvirus insertion mutant genes were derived from plasmids p53wtXbaISP6/T3, p53-21XbaI and p53-238XbaI respectively. The vaccinia H6 promoter was derived from plasmid pRW825 and precisely linked to the 5'-most region of the p53 construction of poxvirus based recombinant viruses expressing wild type and mutant forms of the human p53 gene product. The wild type and containing the vaccinia H6 promoter and the wild type human p53 in vP1101 and vCP207, respectively. These sequences were used : DNA encoding cytokine and/or tumour associated antigen Example 15; Fig 18; 232pp; English.

The sequences given in 96/863-64 represent expression cassettes WPI; 94-263767/32. Cox WI, /note= "Flanking sequence" promoter 109..232 Synthetic. ALVAC(CPpp)p53; poxvirus; antigenic response; immunological response; Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; p53; wild type; mutant; p53wtXbaISP6/T3; p53-21XbaI; p53-238XbaI; Vaccinia H6 promoter/human p53 expression cassette from vCP207. Attenuated recombinant virus used for cancer therapy - comprises (VIRO-) VIROGENETICS CORP. 19-JAN-1994; US-184009. 21-JAN-1993; 04-AUG-1994. WO9416716-A. /note= "Flanking sequence" misc feature misc feature pathogen; ss. vaccinia; H6 promoter; plasmid; pRW825; expression cassette; 22-MAR-1995 21-JAN-1994; U00888 /product= Wild type human /note= "Vaccinia H6 promoter" CDS 233..1414 /\*tag= c 5 AGGCCTTAGAGTTAAAGGATGCCCATGCT 33 Paoletti E, Tartaglia J; us-007115. (first entry) Conservative Location/Qualifiers
1..108 1415..1483 DNA; 1483 BP Score 19; DB 12; Pred. No. 2.07e-01; 0; Mismatches 5. Length 1483; 0 Gaps or P the ٥,

Mar 25 02:41

 $\Box$ 

RESULT
ID Q2
AC Q2
DT 11
DE Mu Query Match 50.0%; Best Local Similarity 82.8%; 1305 aggccttggaactcaaggatgcccaggct 1333 construction of poxvirus based recombinant viruses expressing wild type and mutant forms of the human p53 gene product. The wild type and mutant genes were derived from plasmids p53wtXbaISP6/T3, p53-21XbaI and p53-238XbaI respectively. The vaccinia H6 promoter was derived from plasmid pRW825 and precisely linked to the 5'-most region of the p53 T 14 Q27944 standard; cDNA; 1740 BP Q27944; Mutant p53 polypeptide (Hup53HIS273). gene. Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; p53; wild type; mutant; p53wtXbaISP6/T3; p53-21XbaI; p53-238XbaI; vaccinia; H6 promoter; plasmid; pRW825; expression cassette; viruses, and into NYVAC to give vP1101, vP1096 and vP1098. promoter and the p53 genes may be cloned in to the poxvirus insertion plasmid, ALVAC, to give vCP207, vCP193 and vCP191 recombinant containing the vaccinia H6 promoter and the wild type human p53 in vP1101 and vCP207, respectively. These sequences were used i Cox WI, Paoletti E, Tartaglia J; WPI; 94-263767/32. /\*tag= misc\_feature 11-FEB-1993 (first entry) immunological response, ie. for immunisation against pathogens. Sequence 1512 BP; 379 A; 419 C; 380 G; 334  $\mathrm{T}_i$ viruses may be used in a composition for inducing an antigenic or The sequences given in Q67863-64 represent expression cassettes Example 15; Fig 17; 232pp; English. DNA encoding cytokine and/or tumour associated antigen Attenuated recombinant virus used for cancer therapy -(VIRO-) VIROGENETICS CORP. 21-JAN-1993; US-007115. 19-JAN-1994; US-184009. 21-JAN-1994; U00888. 04-AUG-1994. W09416716-A. misc feature /note= "Vaccinia H6 promoter" CDS 269..1450 promoter /note= "Flanking Synthetic. pathogen; ss. ALVAC (CPpp) p53; Vaccinia H6 promoter/human p53 expression cassette from vP1101. 22-MAR-1995 ე67863; Q67863 standard; /note= "Flanking sequence" /product= Human /\*tag= c /\*tag= 5 AGGCCTTAGAGTTAAAGGATGCCCATGCT 33 The expression cassettes generated by linking the vaccinia H6 24; Conservative (first entry) poxvirus; antigenic response; immunological response; wildtype p53 145..268 Location/Qualifiers DNA; 1512 ВP Pred. No. 2.07e-01 Score 19; <u>,</u>. Mismatches These sequences were used in the DB 12; Length 1512; Indels comprises 0 These Gaps gene 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 82.8%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q51787
Q51787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-1992;
01-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1325 aggcettggaactcaaggatgcccagget 1353
excluding stop codons" US5227293-A.
                                                 /rpt_type= tandem
/note= "can be repeated z times, where z is 1-4,
provided that y+z is 6-12; N stands for
identical or different nucleotides,
                                                                                                                                                                                                                                                                                          provided that y+z is 6-12" repeat_region 4..36
                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mixed oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein; ballast constituent; pro-insulin production; recombinant protein production; HMG CoA reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-1993 (first entry)
Mixed oligonucleotide #19 encodes ballast constituent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence derived from activated p53 oncogene given in the specification has been published by Harlow E. et al. (1985) Molecular and Cellular Biology 5:1601-1610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library was constructed using mRNA extracted from A431 cells (express Hup53HIS273) as described by Harlow E. et al., (1985) J. Virol. 37:1601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present intracellularly at high concns. in mammalian tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant p53 polypeptides encoded by activated p53 oncogenes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 52; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sub ject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         presence of mutant p53 polypeptide in a fluid sample from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing a neoplastic condition in a subject -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 92-300054/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reynolds FH, Sorvillo JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uncogene; tumour; neoplasia;
                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and expression of mutant p53 polypeptide is described, where a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for the early detection and monitoring of neoplastic conditions. In the Experimental Detail section of the specification the cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide conc. and the presence of neoplastic disease provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ONCO-) ONCOGENE SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-1991; US-719172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9213970-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                    repeat_unit
                                                                                                                                                                                                                                                                                                                                               /rpt_type= tandem
/note= "can be repeated y times, where y is 4-11,
                                                                                                                                                                           /*tag= c
                                                                                                                                                                                                                                        /note= "(DCD)11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AGGCCTTAGAGTTAAAGGATGCCCATGCT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1740 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-649566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                4..6
                                                                                                                                                                                                          36..38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The correlation between the measured mutant p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stephenson JR, Zeheb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.07e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1740,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by detecting nple from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Mar 25 02:41

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В
                                                                         Query Match 47.4%;
Best Local Similarity 18.8%;
Matches 6; Conservative
                                                                                                                          Claim 9: Column 30; 22pp; English.

Claim 9: Column 30; 22pp; English.

This preferred mixed oligonucleotide encodes a ballast constituent and is inserted between a regulatory region and the structural gene encoding a desired protein, esp. pro-insulin. The short ballast component improves protease resistance of the fusion protein while still allowing the desired protein to adopt its correct conformation prior to cleavage of the ballast constituent.

Sequence 39 BP; 1 A; 11 C; 1 G; 1 T;
                                                                                                                                                                                                                                                                                                                                              13-JUL-1993.
29-AUG-1989; 399874.
29-AUG-1989; US-399874.
23-APR-1992; US-383221.
(GEHO ) GEN HOSPITAL CORP.
(FARH ) HOECHST AG.
Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W; WPI; 93-235119/29.
                                                                                                                                                                                                                                                                                                            Fusion proteins for prodn. of e.g. pro-insulin - comprise gene for desired protein and oligo-nucleotide(s) encoding ballast
Score 18; DB 7; Length 39; Pred. No. 7.47e-01; 19; Mismatches 7; Indels
                                                                       0;
                                                                       Gaps
                                                                          .
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Search completed: Tue Mar 25 02:42:45 1997 Job time : 15 secs.

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Mar 24 11:15 US-08-644-289-1\_rag

Mar 24 11:15

US-08-644-289-1\_rag

(Fig.

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc. MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 24 11:17:33 1997; MasPar time 1.84 Seconds 111.735 Million cell updates/sec

Tabular output not generated.

Title: >US-08-644-289-1
Description: (1-20) from US08644289.pep
Perfect Score: 151

Sequence: 1 SLRPFKALVREKGHRPSHSC 20

Scoring table: PAM 150 Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 20.568; Variance 59.693; scale 0.345

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	Score	Query Match	Length DB		Ħ	Description	Pred. No.
_	151	100.0	20 1	00	R92698	Human wild-type p53 q	8.31e-11
2	60	39.7	247	w	R13252	Murine Cytotoxic Cell	1.53e+01
ω	60	39.7	619	S	R27651	Human calcium channel	
4	60	39.7	993	G	R27650	Human calcium channel	
5	60	39.7	1873 13	-	R73055	Rabbit skeletal calci	
6	60	39.7			P95645	Rabbit seletal muscle	
7	69	39.7	1967	6	R33547	Sequence of the alpha	
œ	60	39.7	2138 1	4	R72607	Human neuronal calciu	1.53e+01
9	60	39.7	2161 1	4	R71002	Human neuronal calciu	
10	60	39.7	2161 1	4	R71001	Human neuronal calciu	
11	60	39.7	2161	9	R33545	Sequence of the alpha	
12	60	39.7	2163 1	4	R71003	Human neuronal calciu	1.53e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
51	51	51	51	51	51	52	52	52	52	53	53	53	53	53	53	53	53	53	53	53	53	54	54	54	54	54	54	54	55	57	57	57
33.8	33.8	33.8		33.8		34.4	34.4	34.4	34.4	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.8	35.8	35.8	35.8	35.8	35.8	35.8	36.4	37.7	37.7	37.7
1196 16	567 18		305 17	118 13	118 17	690 3	436 17		223 7		2019 13	1989 18	1989 18		1977 18	1835 18		1011 18	399 7	148 6	99 13		2813		677 18		256 15	237 4		3164 16		349
6 R75189		R76578		8 R74338		3 R15482	7 R98146	7 R98143	7 R37573	2 R06584	3 R67913	8 R92317	8 R99640	8 R99639	8 R99641		R51264		-	6 R29180	3 R72089	3 P60462	3 P60053			_		4 R20509		6 R94346	3 R13944	4 R20784
Osteoinductive retrov	(C)		AFT-1 (Arabidopsis fo	Helicobacter pylori h	Heat shock protein HS	Protein encoded by OR		Tne DNA polymerase.			dium char	nervous	l nervous	l nervous	•	nervous	protein	Peripheral nervous sy		Astrovirus serotype A	AbI SH2 region.		Sequence of von Wille	SA8 virus gB glycopro	Human choline acetylt		reproPR-3.	Human proteinase 3.	Human luteinising hor	Hepatitis GB virus (H	Partial HVT ribonucle	Tulip allylacyl amida
1.35e+02	1.35e+02	1.35e+02	1.35e+02	1.35e+02	1.35e+02	1.07e+02	1.07e+02	1.07e+02	1.07e+02	8.43e+01	8.43e+01	8.43e+01	8.43e+01	8.43e+01	8.43e+01	8.43e+01	8.43e+01	8.43e+01	8.43e+01	8.43e+01	8.43e+01	6.64e+01	6.64e+01	6.64e+01	6.64e+01	6.64e+01	6.64e+01	6.64e+01	5.22e+01		3.21e+01	3.21e+01

## ALIGNMENTS

SULT 1
R92698 standard; peptide; 20 AA.
R92698;
03-0CT-1996 (first entry)
Human wild-type p53 gene intron 10 encoded epitope.
Tumour suppressor; p53; alternative splicing; antibody; cancer;
proliferative disorder; psoriasis; prognosis; diagnosis; cell cycle.
Homo sapiens.
CA2150994-A.
15-DEC-1995.
05-JUN-1995; 150994.
14-JUN-1994; US-259612.
(HEAL-) HEALTH RES INC.
Kulesz-Martin MF;
WPI; 96-140137/15.
New antibodies specific for alternatively spliced mammalian p53 -
useful in diagnosis or prognosis of cancer, and for establishing
individual treatment regimes.
Claim 5; Page 25; 40pp; English.
R92698 is an epitope from intron 10 of the human p53 gene. Antibodies
directed against this sequence in an alternatively spliced p53 are
useful in diagnosis and prognosis of human cancer. Antibodies against
the epitope may be used in the study of p53 and alternatively spliced
p53 (p53as) and their expression, when the antibodies are injected
into cells they may cause cell cycle arrest. Vectors contg. p53as
cDNA may be used in gene therapy of cancers and other proliferative
disorders e.g. psoriasis.

SS

Sequence

20 AA;

Best Query Match

y Match 100.0%; Local Similarity 100.0%;

Score 151; DB 18; Pred. No. 8.31e-11;

Length

Matches

20;

Conservative

0;

Mismatches

0;

Indels 20;

0

Gaps

0

channel ligands

N-PSDB; Q29271. WPI; 92-333446/41.

calcium flux assays to screen for neurone-specific calcium Cloned human neuronal calcium channel sub-types - useful in

S g

1 slrpfkalvrekghrpshsc

SLRPFKALVREKGHRPSHSC

20 20

Murine Cytotoxic Cell Protease-1.
mouse; CCP-1 inhibitor; cytotoxic T-lymphocytes; ss.

Location/Qualifiers

Gaps

0

R13252;

11-OCT-1991 (first entry)

R13252 standard; Protein; 247 AA

Mar 24 11:15

US-08-644-289-1 rag

4

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RESULT
ID R2
AC R2
DT 03
DE Hu
KW P1
OS Hc
PN EE
PN EE
PD 07
PF 27
PR 04
PA (E
23-MAR-1992; 104970.
04-APR-1991; DE-110785.
(FARB ) BAYER AG.
Franz J, Rae P, Unterbeck A, Weingaertner
                                                                      EP-507170-A.
                                                                                                                                                    R27651 standard; Protein; 619 AA
                                                        07-OCT-1992.
                                                                                     Homo sapiens.
                                                                                                 Plasmid pCA9.3; Ca-flux assay.
                                                                                                               Human calcium channel 27980/13.
                                                                                                                           03-MAR-1993 (first entry)
                                                                                                                                          R27651;
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254 lrplrainrakglkhvvqc

Matches

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Conservative

4:

Mismatches

7:

Indels

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Gaps

0

S 뭉

ω

RPFKALVREKGHRP SHSC

20

32 rpymallsikdqqpeaic 49

Best

Local

Similarity

39.7%; ilarity 38.9%; Conservative

Pred.

Mismatches

6;

Indels

0

Score 60; DB 3; I Pred. No. 1.53e+01;

DB 3; Length 247;

Sequence

247 AA;

Matches Query Match

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protein was used to design peptides which competitively inhibit the protease. See also Q12863-6 and R13254-R13262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of CCP-1 was predicted from the cDNA sequence. The structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The CCP-1 coding sequence was isolated from the cytotoxic T-cell line MTL 2.8.2 generated from CBA/J mice. The amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                        RESULTION ACCORDANCE TO THE PROPERTY ACCORDANCE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
Query Match 39.7%;
Best Local Similarity 42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.7%;
Best Local Similarity 42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human neuroblastoma cell line, hippocampus, frontal and temporal cortex and visual cortex CDNA banks were screened with a probe containing carp skeletal muscle Ca-channel cDNA. The cDNA clone pCA9.3 was sequenced. The 5'end of the clone begins directly after Domain I (amino acid 337) and the 3'end is at amino acid 922. The
                                                                                                                                          and IV and part of the C-terminus coding sequence. The human neuronal calcium channel protein can be used for screening for Ca channel ligands (agonists or antagonists). See also Q29259-Q29275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calcium flux assays to screen for neurone-specific calcium channel ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Franz J, Rae P, Unterbeck A, Weingaertner B; WPI; 92-333446/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R27650 standard; Protein; 993 AA
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 78-82; 101pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloned human neuronal calcium channel sub-types - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q29270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1992; 104970.
04-APR-1991; DE-110785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP-507170-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc difference 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pCA3; Ca-flux assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human calcium channel 27980/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal calcium channel protein can be used for screening for Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 83-85; 101pp; German.
                                                                                                                                                                                                                                                   Domains II and III. The clone comprises the complete Domains III
                                                                                                                                                                                                                                                                                                                          containing carp skeletal muscle Ca-channel cDNA. The cDNA clone
                                                                                                                                                                                                                                                                                                                                                               cortex and visual cortex cDNA banks were screened with a probe
                                                                                                                                                                                                                                                                                                                                                                                                    Human neuroblastoma cell line, hippocampus, frontal and temporal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc_difference 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      channel ligands (agonists or antagonists). See also Q29259-Q29275
                                                                                                                                                                                                                                                                                    pCA3 was sequenced. The 5'end of the clone lies between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-0CT-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "corresponds to nonsense codon TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "corresponds to nonsense codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 lrplrainrakglkhvvqc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LRPFKALVREKGHRPSHSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 AA;
                                                                                                               993 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB 5; Lengu.
Pred. No. 1.53e+01;
   Score 60; DB 5; I
Pred. No. 1.53e+01;
                                 Length 993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
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DNA vectors, and inhibitors of cytotoxic cell protease - f treatment of auto-immune diseases e.g. pernicious anaemia, rheumatoid arthritis, allo-graft rejection etc.

Claim 5; Fig 3; 62pp; English.

Bleackley RC, Lobe CG, Paetkau VH, James MN, Murphy M; WPI; 91-237989/32.

N-PSDB; Q12862.

RESULT
AC AN ACCORDANCE OF PURE ACCORDANCE OF PURE

(SERA-) SERAGEN INC. 19-JAN-1990; US-467880 17-JAN-1991; U00340.

25-JUL-1991. WO9110685-A. /label= CCP-1

/label= signal\_peptide Protein 21..247

Peptide Mus musculus.

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2 LRPFKALVREKGHRPSHSC

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Mar 24 11:15

Modified site 1777, Modified site 1777, Modified site 1772 Modified site 1/1.
Modified site 1/1.
/label= see above Modified site 191
| Modified site 191
| Modified site 1964 Region 43:
/label= see above
Region 46
/label= see above Modifieu ..../label= see above 1757 Region /label= see above 433..451 Protein /label= see above 121..139 /label= see above R73055 standard; Protein; 1873 AA.
R73055;
02-NOV-1995 (first entry)
Rabbit skeletal calcium channel (alpha)1-subunit.
calcium channel; (alpha)1 subunit. /note= "In Tanabe et al" Misc\_difference 1835 Region 4 /label= see above Region 19 /label= see above Region 10 /label= see above Region 12 /label= see above Modified site 1502 Modified\_site 687 /label= Potential N-glycosylation site Modified\_site 257 /note= "In Tanabe et al"
Misc\_difference 1815 /label= transmembrane region Protein 89..108 /label= potential cAMP-dependent phosporylation /label= see above Modified site /note= "In Tanabe et al" Misc\_difference 1808 /label= IIF7 monoclonal antibody epitope Oryctolagus cuniculus. Region /label= see above /label= see above /label= see above /label= Ala /label= Ala /label= Thr Region 467..486 52..70 495..513 199..218 950..1100 161..179 Location/Qualifiers

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902 lrplrainrakglkhvvqc 920

Query Match 39.7%; Best Local Similarity 42.1%; Matches 8; Conservative

Score 60; DB 13; Length 1873; Pred. No. 1.53e+01; 4; Mismatches 7; Indels 0;

Gaps

0

		E E E E E E E E E E E E E E E E E E E
(SALK ) SALK INST B. Brenner R, Ellis SI		Region /label= Region /label= Region /label= Region
SALK INST B SALK INST B R, Ellis S 161088/21. 2637978. 2637978. 264079 S 264070 S 264070 S 264070 S 264070 S 264070 S 26	abo	see above 5 see above 6 see above 8
(SAIK) SAIK INST BIOTECHNOLOGY IND ASSOC. Brenner R, Ellis SB, Harpold MM, Schwartz A, Williams ME; WPI; 95-161088/21.  NN-PSDB; Q87978.  NN-PSDB; Q87978.  NN-PSDB; Q87978.  NN-PSDB; Q87978.  NN-PSDB; Q87978.  The colk sequence Q19798 is consistent with an approx 6,500 nt DHP receptor (alpha)1 mRNA. It is 94% identical to the cDNA sequence encoding the DHP receptor reported by Tanabe et al., Nature, 328:313-318, 1987. Nt differences were identified at 33 posns, of which three (see FT) also result in AA changes (see R73055 FT). The deduced AA sequence yields a calculated Mr of 212,413,in contrast to the observed Mr 155K-170K, previously reported by others using SDS polyacrylamide gel electrophoresis. The AA sequence is 99.8% identical to that described by Tanabe et al. It contains four internal repeated sequence regions. It has been proposed that the segments of the four internally repeated regions represent 24 transmembrane segments. A eukaryotic cell expressing a chimaeric cDNA is claimed, in which the first cDNA is selected from the gp. consisting of cDNA that encodes a protein that has the AA sequence in R73055 but with the Tanabe et al substitutions indicated in FT. Sequence 1873 AA;	1079 2 2 1 1 1 0 3 5 6 3	524542 ve 562581 ve 637661 ve 800818

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2 LRPFKALVREKGHRPSHSC

Mar 24 11:15

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Sequence

1967 AA;

encodes an alternative exon

for the IV S3 transmembrane domain.

US-08-644-289-11rag

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S
              Numerous alpha 1C-specific DNA clones were isolated. Characterisation of the sequence revealed the alpha 1C coding sequence, the alpha 1C initiation of translation sequenc, and an alternatively spliced region of alpha 1C. Q37814 and Q37815 encode
                                                                                                                                                                                                      14-AUG-1992; U06903.
15-AUG-1991; US-745206.
10-APR-1992; US-868354.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                          DNA encoding specific human calcium channel sub-units - used for
                                                                                                                                                          WPI; 93-093936/11.
                                                                                                                                                                                        Brenner R,
                                                                                                                                                                                                                                                                      04-MAR-1993.
                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                               Sequence of the alpha 1C human calcium channel subunit. Human calcium channel subunit; diagnosis; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                R33547 standard;
                                                                              Disclosure; Page 102-109; 150pp; English.
                                                                                            diagnosing Lambert Eaton syndrome
                                                                                                                                           N-PSDB; Q37813.
                                                                                                                                                                         Williams ME;
                                                                                                                                                                                                                                                                                      м09304083-A.
                                                                                                                                                                                                                                                                                                                   Lambert Eaton syndrome.
                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   R33547;
                                                                                                             identifying calcium channel agonists and antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
possible amino terminal ends of the alpha 1C protein. Q37816
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRPFKALVREKGHRPSHSC
                                                                                                                                                                                        Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                               Protein; 1967
                                                                                                                                                                                        Feldman DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                Ä
                                                                                                                                                                                     Harpold
                                                                                                                                                                                         ¥,
                                                                                                                                                                                           Mccue
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Human neuronal calcium channel subunit alpha  ${\tt ID}$  including exon encoding the  ${\tt IS6}$  transmembrane domain.

30-NOV-1995 (first entry)

Calcium channel subunit; antagonist; agonist; diagnosis;

RESULT Ş Q 밁 Best Matches Query Match 1003 lrplrainrakglkhvvqc 1021 translation and an alternatively spliced region. Q84655 sets forth one alpha lc coding sequence (alpha lc-1) and R71003 sets out its deduced AA sequence. Q87834 and R72607 set out another obtaining agonists and antagonists Claim 34; Page 260-269; 285pp; English. 05-NOV-1993; US-149097. (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC. (Ellis SB, Gillespie A, Harpold MM, Mccue R71002 standard; Protein; 2161 R71002; and/or inserting the alternative exon in the appropriate location (see Q84655 FT). In addition, a nt. sequence (see Q84655 alpha ic variants can be constructed by selecting alternative amino terminal ends in place of the ends in Q84655 and Q87834 splice variant, designated alpha 1c-2. Q84656 encodes an Numerous alpha lc-specific cDNA clones were isolated in order to Homo sapiens. Human neuronal calcium channel subunit alpha 1c-2. Calcium channel subunit; antagonist; agonist; diagnosis; 01-DEC-1995 (first entry) R72607; R72607 standard; Protein; 2138 Sequence alternative exon for the IV S3 transmembrane domain. Other characterise the alpha 1c coding sequence, the initiation developing prods. for studying calcium channels, e.g. N-PSDB; Q87834. WPI; 95-090900/12. splice variant. FT) can be deleted or inserted to produce an alternative alpha DNA encoding human calcium channel sub-unit(s) - used WO9504822-A. 11-AUG-1993; US-105536. 1-AUG-1994; Lambert Eaton Syndrome. 6-FEB-1995. Match 39.7%; Local Similarity 42.1%; 2 LRPFKALVREKGHRPSHSC 2 LRPFKALVREKGHRPSHSC = :: 8 2138 AA; Conservative 20 Score 60; DB 14; Lenc ; Pred. No. 1.53e+01; "'cmatches 7; A A Æ, Length 2138; Williams ME; Indels 0; Gaps <u>.</u>

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902 lrplrainrakglkhvvqc 920

Matches

00

Conservative

Query Match 39.7%; Best Local Similarity 42.1%;

39.7%;

Score 60; DB 1; Pred. No. 1.53e+01

Length 1873;

Mismatches

Indels

0; Gaps

0

probes.

Sequence

1873 AA;

Disclosure; page 16-1 to 18-3; 68pp; English. Also used to diagnose Lambert-Eaton syndrome by reacting test serum with alpha-1 and alpha-2 subunits. Labelled fragments can be used as

agonist or antagonist activity

04-APR-1988; 001408. 04-APR-1988; US-176899. (SALK) Salk Inst for Biol Stud.

W08909834-A.

19-OCT-1989.

Sylvilagus (rabbit). Skeletal muscle Rabbit seletal muscle alpha-1 sub-unit gene product.

В

1027 lrplrainrakglkhvvqc 1045

Matches

<u>«</u>

Conservative

4.

Mismatches e 60; DB 6; I . No. 1.53e+01;

0;

Gaps

0

Pred. Score

Length 1967

Query Match 39.7%; Best Local Similarity 42.1%;

21-MAR-1990 (first entry)

P95645 standard;

protein; 1873

A

P95645;

Ellis SB, Williams ME, Harpold MM, Schwartz A, Sartor J; WPI; 89-324236/44.

N-PSDB; N91778.

New DNA encoding alpha-2 subunit of animal calcium channel - also new

protein product and eukaryotic cells for testing cpds. for calcium

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human alpha 1D subunit was obtd. Full-length clones were then constructed by ligating partial clones. Q84653 shows the nt sequence of the CNN encoding the alpha 1D subunit. The Albha 1D protein has a calculated Mr of 245,163. It contains four putative internal repeated sequence regions which represent 24 putative transmembrane segments. It mediates DHP-sensitive high-voltage, long-lasting
                                                   (SALK ) SALK INST BIOTECHNOLOGY IND Ellis SB, Gillespie A, Harpold MM, WPI; 95-090900/12.
                                                                                                                                                                        Homo sapiens.
W09504822-A.
                                                                                                                                                                                                                                                                           R71001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calcium channel activity. Q84654 shows an alternative exon encoding the IS6 transmembrane domain. The difference occurs in AAs 373-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-1993; US-105536.
05-NOV-1993; US-149097.
DNA encoding human calcium channel sub-unit(s) - developing prods. for studying calcium channels,
                                                                                                    11-AUG-1993; US-105536.
05-NOV-1993; US-149097.
                                                                                                                                                                                                                      Calcium channel subunit; antagonist; agonist; diagnosis;
                                                                                                                                                                                                                                         Human neuronal calcium channel subunit alpha 1D.
                                                                                                                                                                                                                                                                                           R71001 standard; Protein; 2161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clones, which were then employed for screening until a sufficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe to screen a cDNA library of human neuroblastoma cell line INM32, to obtain clone alphal.36, This close was used as a probe to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The alpha 1D subunit cDNA has been isolated using fragments of the rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obtaining agonists and antagonists Disclosure; Page 126-127; 285pp; Er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 95-090900/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9504822-A.
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                                    N-PSDB; Q84653.
                                                                                                                                      11-AUG-1994; U09230.
                                                                                                                                                        16-FEB-1995.
                                                                                                                                                                                                         Lambert Eaton Syndrome.
                                                                                                                                                                                                                                                           30-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        series of clones to span the length of the nt seuence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scren additional IMR32 cell cDNa libraries to obtain overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developing prods. for studying calcium channels, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human calcium channel sub-unit(s) - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q84654.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= encoded by alternative exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-FEB-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                989 lrplrainrakglkhvvqc 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 39.7%;
Local Similarity 42.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2161 AA;
                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
n calcium channel sub-unit(s) - used
for studying calcium channels, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 60;
Pred. No.
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                                                                                    ASSOC.
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                                                                   Мссие
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Best Local Similarity 42.1%;
                Query Match
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                                                                                                                                                    clones which were then employed for screening until a sufficient series of clones to span the length of the nucleotide sequence
                                                                                                                                                                                        The alpha ID subunit cDNA was isolated using fragments of the rabbit skeletal muscle calcium channel alpha I subunit cDNA as a probe to screen a cDNA library of a human neuroblastoma cell line, IMR32, to obtain clone alpha 1.36. This clone was used as a probe to screen additional IMR32 cell cDNA libraries to obtain overlapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constructed by ligating partial clones. Q84653 shows the nt sequence of the cDNA encoding the alpha 1D subunit. The Alpha 1D protein has
                                                         Sequence
                                                                           transmembrane domain of the alpha 1D subunit. The alpha 1D protein has a calculated Mr of 245,163.
                                                                                                                                  encoding the human alpha 1D subunit were obtained, see Q37811.
                                                                                                                                                                                                                                                                                                                                                                                                                            Brenner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human calcium channel subunit; diagnosis; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of the alpha 1D human calcium channel subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                segments. It mediates DHP-sensitive high-voltage, long-lasting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a calculated Mr of 245,163. It contains four putative internal
                                                                                                                Q37812 provides the sequence of an alternative exon encoding the IS6
                                                                                                                                                                                                                                                                                     diagnosing Lambert Eaton syndrome Disclosure; Page 93-101; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q37811.
                                                                                                                                                                                                                                                                                                                                                                                                          Williams ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9304083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeated sequence regions which represent 24 putative transmembrane
                                                                                                                                                                                                                                                                                                                                               DNA encoding specific human calcium channel sub-units - used
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                                                                                                                                                                                                                                                                                                                                                                                                                        (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Brenner R, Ellis SB, Feldman DH, Harpol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-AUG-1991; US-745206.
10-APR-1992; US-868354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1992; U06903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lambert Eaton syndrome.
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                                                                                                                                                                                                                                                                                                                             dentifying calcium channel agonists and antagonists and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
 39.7%;
42.1%;
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Score
Pred.
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Pred. No. 1.53e+01;
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 N 60
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   DB 6; L
1.53e+01;
                   Length 2161;
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Best Local Similarity

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Matches

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Conservative

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Mismatches

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989 lrplrainrakglkhvvqc 1007

2 LRPFKALVREKGHRPSHSC

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AC DT DE CON PR PR PR PR J03290190-A. 19-DEC-1991. 06-APR-1990; 091565. 06-APR-1990; JP-091565. Tulippa. R20784 standard; Protein; 349 AA. Chemical selection; herbicide resistance. Tulip allylacyl amidase. R20784; 12-MAY-1992 (first entry) NORINSHO

> Ş В

> > 415 lrpysqlird 424

|||: |:|: 2 LRPFKALVRE 11

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2 LRPFKALVREKGHRPSHSC 20

맑 Query Match 39.7%; Best Local Similarity 42.1%; Matches obtaining agonists and antagonists
Disclosure; Page 127-137; 285pp; English.
Numerous alpha 1c-specific cDNA clones were isolated in order to characterise the alpha 1c coding sequence, the initiation of translation and an alternatively spliced region. Q84655 sets 1028 lrplrainrakglkhvvqc 1046 and/or inserting the alternative exon in the appropriate location (see Q84655 FT). In addition, a nt. requence (see Q84655 FT) can be deleted or inserted to produce an alternative alpha lo forth one alpha 1c coding sequence (alpha 1c-1) and R71003 sets out its deduced AA sequence. Q87834 and R72607 set out another WPI; 95-090900/12. 05-NOV-1993; US-149097. Calcium channel subunit; antagonist; agonist; diagnosis; sequence splice variant amino terminal ends in place of the ends in 084655 and 087834 alpha lc variants can be constructed by selecting alternative alternative exon for the IV S3 transmembrane domain. Other splice variant, designated alpha 1c-2. Q84656 encodes an developing prods. for studying calcium channels, e.g. DNA encoding human calcium channel sub-unit(s) - used N-PSDB; Q84655. Ellis SB, Homo sapiens. WO9504822-A. Human neuronal calcium channel subunit alpha 1c-1. 30-NOV-1995 R71003; R71003 standard; Protein; 2163 AA. (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC. Ellis SB, Gillespie A, Harpold MM, Mccu Lambert Eaton Syndrome. l1-AUG-1993; US-105536. 11-AUG-1994; U09230 .6-FEB-1995. <u>«</u> Gillespie A, 2163 AA; (first entry) Conservative Score 60; DB 14; Length 2163; Pred. No. 1.53e+01; 4: Mismatches Mccue AF, 7; Indels 0; Williams for M Gaps ٥.

Ş B Matches Query Match 37.7%; Best Local Similarity 50.0%; Matches Query Match 37.7%; Best Local Similarity 40.0%; SDS-PAGE. The amino acid sequence was determined and the crude protein used to prepare rabbit anti-allylacyl amidase serum to screen a cDNA library, constructed in lambda gtll using thip bulb for use in live vaccines as it is apathogenic and non-oncogenic. See also Q13668. Sequence  $553~\mathrm{AA}_{\mathrm{F}}$ New herpes recombinants - useful as vaccines against human and animal viral conditions, e.g. fowl pest, coccidiosis and 07-MAR-1991; 400634. 12-MAR-1990; FR-003105. EP-447303-A. Newcastle disease; recombinant poultry virus vaccine. Turkey herpes virus strain FC 126. R13944; the entire RR2 gene. Knowledge of the RR2 small sub-unit sequence is exploited in the construction of recombinant vaccines. A heterologous N-PSDB; Q13430. Partial HVT ribonucleotide reductase large subunit RR1. R13944 standard; Protein; 553 Sequence poly A + RNA. The base sequence and corresp. amino acid sequence Crude allylacyl amidase was prepd. from tulip bulbs and purified Disclosure; Fig 3; 11pp; Japanese. DNA encoding tulip allacyl amidase - useful in chemical selection and N-PSDB; Q20497. bronchitis, etc. is inserted into the RR2 gene. The HVT is suitable Newcastle disease, avian anaemia, colibaccillosis, avian infectious WPI; 91-275886/38. Rey-Senelonge A, Kohen G; 27-NOV-1991 hydroxyapatite chromatography. The purified protein was partially digested by lysyl endopeptidase and the protein fragment sept. by prodn. of herbicide resistant plants. WPI; 92-045622/06. sequence coding for an appropriate immunogen to protect against e.g. from a genomic DNA clone which was isolated because it contained This sequence is the C-terminal region of HVT RR1. It was deduced Disclosure; Page 13-14; 22pp; French. pasteurellosis (RHON-) RHONE MERIEUX SA. were then determined. by dialysis, DEAE cellulose chromatography, [8-SEP-1991. 6 KALVREKGHRPSHSC 20 5 kdivrqtvkppahac 19 5 6. 349 AA; Conservative Conservative (first entry) Pred. No. 3.21e+01; Score 57; Score 57; DB 4; I Pred. No. 3.21e+01; 3; Mismatches 4; Mismatches A DB 3; gel filtration and Length 553; 5; Length 349; 2; Indels Indels <u>.</u> ·, Gaps Gaps <u>.</u> ç

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RESULT

ID 88

AC DT 028

AC DT 0 밁 Query Match 37.7%; Best Local Similarity 54.5%; Matches 6; Conservative, 17-AUG-1995. 14-FEB-1995; U02118. 14-FEB-1994; US-196030. 13-MAY-1994; US-242654. 29-JUL-1994; US-283314. 23-NOV-1994; US-344190. 23-NOV-1994; US-344185. 1980 rrrgyrprhac 1990 Simons JN;
WRI; 95-293123/38.
WRI; 95-293123/38.
N-SDB; T00129.
Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for diagnosis and therapy of hepatitis GB virus
Example 9; Pages 343-357; 661pp; English.
Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV infected tamarin plasma, using standard procedures, was used to prepare a lambda phage HGBV cDNA library. Clones were rescued from the lambda phage, searched against a sequence database and found to be unique HGBV sequences. The clones were then used to assemble the sequences T00129/30 (GB contig A and B) which encode the proteins R94345-47 (the 3 possible coding strand reading frames) and R82072, respectively. Reagents which comprise the HGBV DNA, or its protein prods. can be used for the diagnosis, therapy or in a vaccine to prevent HGBV infection. R94346;
02-UUL-1996 (first entry)
Hepatitis GB virus (HGBV) clone GB contig A protein prod.
Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine;
reagents; non-A; non-B; non-C; non-D; non-E; clone; GB contig A;
tamarin; infected plasma; lambda phage; cDNA library. Buijk SL, Dawson GJ, Desai SM, Erker JC, Leary TP; Muerhoff AS, Mushahwar IK, Pilot-Matias TJ, Schlauder GG; R94346 standard; Protein; 3164 AA. codons in T00129" W09521922-A2. (ABBO ) ABBOTT LAB.
Buijk SL, Dawson GJ, Desai SM, Erker JC, Leary TP, 27-JAN-1995; US-344557. /note= "others correspond to degenerate or STOP Misc\_difference 1..3164 Hepatitis GB virus. 10 REKGHRPSHSC 20 3164 AA; Location/Qualifiers Score 57; DB 16; Length 3164; Pred. No. 3.21e+01; 2; Mismatches 3; Indels 0; Gaps 0

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Search completed: Mon Mar 24 11:17:44 1997 Job time : 11 secs.

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US-08-644-289-1.rsp

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\* (MT)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 24 11:18:31 1997; MasPar time 1.95 Seconds 190.205 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-644-289-1 (1-20) from US08644289.pep 151 1 SLRPFKALVREKGHRPSHSC 20

Scoring table: PAM 150 Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot33
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Database:

Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 28.995; Variance 36.679; scale 0.791

# SUMMARIES

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58	59	59 59	60	60	60	60	60	61	62	64	Score
38.4	39.1	39. <b>7</b> 39.1	39.7	39.7	39.7	39.7	39.7	40.4	41.1	42.4	Query Match
531	392	2171 299	1873	1852	466	256	247	231	164	1166	Length DB
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G11A_ORYSA	NOLC RHIFR	CICC_RABIT	CIC1_RABIT	CICI CYPCA	HEMZ ARATH	YRDA ECOLI	GRAB MOUSE	RM05 PROWI	X16 HUMAN	ADDB_BACSU	ID
PROTEIN KINASE GliA (	NOLC PROTEIN.	DIHYDROPRYRIDINE-SENS PUTATIVE MITOCHONDRIA	DIHYDROPRYRIDINE-SENS	DIHYDROPRYRIDINE-SENS	FERROCHELATASE, CHLOR	HYPOTHETICAL 28.4 KD	GRANZYME B (G, H) PRECU	MITOCHONDRIAL 60S RIB	PRE-MRNA SPLICING FAC	ATP-DEPENDENT NUCLEAS	Description
3.53e+00	2.30e+00	1.49e+00 2.30e+00	1.49e+00	1.49e+00	1.49e+00	1.49e+00	1.49e+00	9.57e-01	6.13e-01	2.47e-01	Pred. No.

# ALI GNMENTS

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SO SERVICE DE LA LA LA LA SERVICE DE LA CONTROL DE LA CONT S 맑 S Query Match Best Local Similarity Matches Query Match 42.4%; Best Local Similarity 69.2%; X16 HUMAN P23152; 01-NOV-1991 01-NOV-1991 (REL. 01-FEB-1994 (REL. REPEAT SIMILAR REPEAT DOMAIN DOMAIN DOMAIN -!- INDUCTION: BY SEKUM, IN A LIBER TO MOTHE (RNP). -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN LINES; HIGH, IN TESTIS, BRAIN AND SPILEN; AYANE M., PREUSS U., KOEHLER G., NIELSEN P.J.; NUCLEIC ACIDS RES. 19:1273-1278(1991). ZAHLER A.M., LANE W.S., STO GENES DEV. 6:837-847(1992). PRE-MRNA SPLICING SEQUENCE NUCLEAR PIR; S14016; S14016. EMBL; X53824; G55440; -. EMBL; L10838; G338484; -. -!- FUNCTION: MAY BE INVOLVED IN RNA PROCESSING IN RELATION WITH MEDLINE; 91232908. SPECIES=MOUSE MEDLINE; SPECIES=HUMAN; EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; HOMO SAPIENS (HUMAN), X16. SEQUENCE PROSITE; PS00030; SEQUENCE FROM N.A. SEQUENCE FROM N.A. SUTHERIA; PRIMATES. 329 reihalvrekgyr 341 NOT DETECTABLE IN LIVER AND KIDNEY.
INDUCTION: BY SERUM, IN A TISSUE CULTURE. CELLULAR PROLIFERATION AND/OR MATURATION. RPFKALVREKGHR 15 PROTEIN; 92249775. 9 1166 (REL. 64 AA; 46 105 Conservative Conservative STANDARD; A, RNA-BINDING; 20, CREATED)
20, LAST SEQUENCE UPDATE)
28, LAST ANNOTATION UPDATE)
FACTOR SRP20 (X16 PROTEIN). RNP 1 41.1%; 50.0%; 53 164 164 133 164 164 19329 134631 AND MUS MUSCULUS (MOUSE) STOLK J.A., ₹ ¥ Score 64; DB 1; Length 1166; Pred. No. 2.47e-01; Pred. No. 6.13e-01; Score 62; ; MRNA SPLICING; REPEAT.
RNA-BINDING (RNP1) (BY SIMILARITY).
ARG/LYS-RICH (HIGHLY BASIC; MAY BE INVOLVED IN NUCLEIC ACIDS BINDING).
2 X APPROXIMATE REPEATS, BASIC. TO PROTAMINES. 531E77C2 CRC32; PRT; Mismatches Mismatches 91EEB84F CRC32; ROTH M.B.; 164 AA. DB 9; Length 164; THYMUS AND PRE-B CELL VERY LOW IN HEART AND Ψ 2; Indels Indels 0. 0 Gaps Gaps 0 0

Mar 24 11:16 US-08-644-289-1.rsp

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Ş В Query Match Best Local S Matches 01-NOV-1995 01-NOV-1995 01-NOV-1995 20-MAR-1987 01-NOV-1995 GRAB\_MOUSE P46749; MEDLINE; 86284960.

BRUNET J.F., DOSSETO M., DENIZOT F., HAQQI T.M., FERRIER P., NABHOLZ M., LUCIANI M.F., GOLSTEIN P.; RM05 MCFADDEN G., BLEACKLEY R.C.; MEDLINE; 86208120. LOBE C.G., FINLAY B.B., P SCIENCE 232:858-861(1986) GRANZYME B (G, H) PRECURSOR (EC 3.4.21.79) (CYTOTOXIC CELL PROTEASE 1) P04187; RIBOSOMAL PROTEIN; MITOCHONDRION EMBL; U02970; G467861; WOLFF G., PLANTE I., LANG B.F. J. MOL. BIOL. 237:75-86(1994). MEDLINE; 94180393. WOLFF G., PLANTE I STRAIN=263-11; CHLOROPHYCEAE; CHLOROCOCCALES; EUKARYOTA; PLANTA; PHYCOPHYTA; MITOCHONDRION. PROTOTHECA WICKERHAMII. RPL5. MITOCHONDRIAL SEQUENCE FROM N.A. BIOCHEMISTRY 27:6941-6946(1988). MEDLINE; 89062424. EUTHERIA; RODENTIA. EUKARYOTA; METAZOA; MUS MUSCULUS (MOUSE). SEQUENCE PROSITE; PS00358; RIBOSOMAL\_L5 -!- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS. SEQUENCE FROM N.A. NATURE 322:268-271(1986) SEQUENCE FROM N.A. SEQUENCE FROM N.A. (CCP1) (CTLA-1) (FRAGMENTIN 20-MAR-1987 -!- SUBCELLULAR LOCATION: MITOCHONDRIAL. 88 lpaftalemitgqkpkytc 106 2 PROWI LRPFKALVREKGHRPSHSC Similarity 7; 7 (REL. 04, CREATED)
7 (REL. 04, LAST SEQUENTS (REL. 32, LAST ANNO 231 AA; (REL. (REL. (REL. AL 60S Conservative STANDARD; STANDARD; . 32, CREATED)
. 32, LAST SEQUENCE UPDA
. 32, LAST ANNOTATION UP
. 32, LAST ANNOTATION UP 36.8%; 26584 CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; 40.4%; DUGGAN B., LANG B.F., LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) LAST ANNOTATION UPDATE) LAST SEQUENCE UPDATE) PARANCHYCH W., DENIZOT F., 20 MW; 2). Score 61; DB 8; I Pred. No. 9.57e-01; E827E483 CRC32; OOCYSTACEAE. CHLOROPHYTA KUECK U., EHRMAN Mismatches , MATTEI M.G., CLARK W. SCHMITT-VERHULST A.M., 247 231 ; PAETKAU V.H., BLEACKLEY R.C.; A A BURGER LETELLIER (GREEN ALGAE); Length 231; <u>∞</u> G.; CLARK W.R., Indels 3 BELL <u>.</u> ۲, Gaps 0

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                                                                                                                                                                                                                    Matches
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Best Local Similarity 38.9%;
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MEDLINE; 87215932.
MASSON D., TSCHOPP J.;
CELL 49:679-685(1987).
                                         01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                        DISULFID
CARBOHYD
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P45770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X04072; G50587; -.
EMBL; M12302; G309154; -.
EMBL; M22526; G201027; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. STRONGEST TO OTHER GRANZYMES AND TO MAST CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               > MET-|-XAA, SER-|-XAA.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MURPHY M.E.P., MOULT J., BLEACKLEY R.C., GERSHENFELD WEISSMAN I.L., JAMES M.N.G.; PROTEINS 4:190-204(1988).
           ESCHERICHIA COLI.
                      YRDA.
                               HYPOTHETICAL
                                                               01-NOV-1995
                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                    APOPTOSIS;
                                                                                                                                                                                                                                                                                                                                                              HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                              PDB;
                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A00956; PRMSCL.
PIR; A28952; A28952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ASP-|-XAA >> ASN-|-XAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 89184501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE MODELLING.
 PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00135;
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-
                                                                                                                                                   32
                                                                                                                                ω
                                                                                    ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIATED IMMUNE RESPONSES. IT CLEAVES AFTER ASP. MAY BE INVOLVED
                                                                                                                               RPFKALVREKGHRPSHSC
                                                                                                                                         rpymallsikdqqpeaic 49
                                                                                                                                                                                                                                                                                                                                                                                              2CP1; 15-0CT-94.
                                                                                                                                                                                                                                                                                                                                                                                                         B26944; B26944.
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                                                                                                                                                                                                                                                                                                                                                    3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                             SERINE PROTEASE; ZYMOGEN; SIGNAL; T-CELL; CYTOLYSIS;
                                                                                                                                                                                                                   247 AA;
                              (REL.
(REL.
(REL.
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                                                                                     STANDARD;
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188
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                              PROTEIN IN RRND-AROE INTERGENIC REGION (0256)
                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                               20
SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS.
                                                                                                                                                                                  Score 60; DB 4; Length 247; Pred. No. 1.49e+00;
                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                 CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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                                                                                                                                                                                                                                                                                                                   GRANZYME B.
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                                                                                     PRT;
                                                                                                                                                                                                                    E05916CB CRC32;
                                                                                                                                                                         Mismatches
                                                                                     256 AA
                                                                                                                                                                         6
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(BY SIMILARITY).
(BY SIMILARITY).
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                                                 Matches
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ECOGENE; EG12838; YRDA.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
TPANSMEM 13 33 POTENTI
                                                                                                                                                                                                                                  STRAIN=CV. LANDSBERG ERECTA; TISSUE=WHOLE SEEDLINGS;
MEDLINE; 94230447.

SMITH A.G., SANTANA M.A., WALLACE-COOK A.D.M., ROPER J.M.,
LABBE-BOIS R.;
J. BIOL. CHEM. 269:13405-13413(1994).

-!- CATALYTIC ACTIVITY: PROTOPORPHYRIN + FE(2+) = PROTOHEME + 2 H(+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
PLUNKETT G. III;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: TO P.AERUGINOSA FERRIPYOCHELIN BINDING PROTEIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U18997; G606213; -.
                                                                                                             CHAIN
                                                                                                                                                                         EMBL; X73417; G511081; -.
                                                                                                                                                                                                                                                                                                                                       CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                         TRANSIT
                                                                                                                                               PORPHYRIN BIOSYNTHESIS; HEME BIOSYNTHESIS; LYASE; IRON; CHLOROPLAST;
                                                                                                                                                            PROSITE; PS00534; FERROCHELATASE.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE;
                                                                                                                                                                                                                                                                                                                                                               ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
                                                                                                 SEQUENCE
                                                                                                                                    TRANSIT
                                                                                                                                                                                     -!- SIMILARITY: TO OTHER SPECIES FERROCHELATASE.
                                                                                                                                                                                                                         -!- PATHWAY: LAST STEP IN PROTOHEME BIOSYNTHESIS.
                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: PRESENT IN BOTH LEAVES AND ROOTS
                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: CHLOROPLAST
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Local Similarity 42.9%;
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|::| : | || ::||
  FKALVREKGHRPSHSC
                                                                                                                                    PEPTIDE.
                                                            Similarity
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                                                                                                 466 AA;
                                                 Conservative
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                                                                                                466
52032
                                                             39.7%;
43.8%;
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  20
                        25
                                                                                                 MW;
                                                             Score 60; DB 4; Length 466; Pred. No. 1.49e+00;
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Pred. No. 1.49e+00;
                                                                                                FERROCHELATASE.
; 2D3756C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                5;
                                                                                                                        CHLOROPLAST (POTENTIAL)
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                                                 Mismatches
                                                4;
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CICI\_CYPCA STANDARD; PRT; 1852 AA. P23316; 01-AUG-1991 (REL. 19, CREATED) 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE) 01-CCT-1993 (REL. 27, LAST ANNOTATION UPDATE) DHYDROPRYRIDINE-SENSITIVE L-TYPE, SKELETAL M

GRABNER M., FRIEDRICH K., KNAUS H.-G., STRIESSNIG J., STAUDINGER R., KOCH W.J., SCHWARTZ A., GLOSSMANN H.; PROC. NATL. ACAD. SCI. U.S.A. 88:727-731(1991).

SCHEFFAUER F.,

SEQUENCE FROM N.A. TISSUE=SKELETAL MUSCLE; MEDLINE; 91126068.

OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;

SKELETAL MUSCLE CALCIUM CHANNEL

CYPRINUS CARPIO (COMMON CARP).

ALPHA-1 SUBUNIT.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- PTM: MAY NOT BE PHOSPHORYLATED.
-!- TISSUE SPECIFICITY: SKELETAL MUSCLE.

-!- SIMILARITY: TO OTHER CALCIUM CHANNEL ALPHA SUBUNITS

DIHYDROPYRIDINE (DHP), A CALCIUM CHANNEL BLOCKER.
-!- SUBUNIT: THIS L-TYPE CALCIUM CHANNEL IS COMPOSED OF TWO SUBUNITS:
ALPHA-1, AND ALPHA-2.

-!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE EXCITATION-CONTRACTION COUPLING. THE ALPHA-1 SUBUNIT BINDS

CC CC CC CC CC CC CC CC CC CC CC CC CC	CC CC C R P A A A A A A A A A A A A A A A A A A	RESULT ID C AC P DT 0 DT 0 DT 0 DT 0 OC C C C C C C C C C C C C C C C C C C	Db Ma	FI FI SO
	II)  SEQUENCE FROM N.A. TISSUE-SKELETAL MUSCLE; MEDLINE; 87258269. TANABE T., TAKESHIMA H., KANGAMA K., KOJIMA M., M NATURE 328:313-318 (1987) [2] [2] [2] SEQUENCE FROM N.A. TISSUE-SKELETAL MUSCLE; MEDLINE; 88356904. ELLIS S.B., WILLIAMS M.E LEUNG A.T., CAMPBELL K.P. HARPOLD M.M.; SCIENCE 241:1661-1664 (19 PI- FUNCTION: CALCIUM CH EXCITATION-CONTRACTI DIHYDROPYRIDINE (DIP	JLT 8 CICI RABIT STANDARD; P07293; 01-APR-1988 (REL. 07, CREA: 01-APR-1988 (REL. 07, LAST 01-OCT-1993 (REL. 27, LAST DHYDROPRYRIDINE-SENSITIVE ALPHA-1 SUBUNIT. ORYCTOLAGUS CUNICULUS (RAB) EUKARYOTA; METAZOA; CHORDA' EUTHERIA; LAGOMORPHA.	Best Local Simi Matches 8; 9 918 lrplrai    :: : 2 LRPFKAL	MOD_RES MOD_RES MOD_RES MOD_RES SEQUENCE
ALPHA-1, ALPHA-2, B: SUBCELIULAR LOCATION TISSUE SPECIFICITY: TISSUE SPECIFICITY: TO OTHE TO O	ENCE FROM N.A. UB-SKELETAL MUSCILINE; 87258269. BE T., TAKESHIMA ARMA K., KOJIMA M. RE 328:313-318(1) ENCE FROM N.A. UB-SKELETAL MUSCILINE; 88336904. S.S., WILLIAMS G.A.T., CAMPBELL OLD M.M.; OLD M.M.; OLD M.M.; OLD M.M.; SUBCITATION-CONTRI DHYDROPYRIDIME SUBUNIT: THE L-T	REL. 07, 88 (REL. 07, 93 (REL. 07, 93 (REL. 27, 94 (RIL. 27, 95 (REL.	Z 5 1	407 1471 1523 1523 1738 E 1852 A
ALPHA-1, ALPHA-2, BETA AND SIBCELLIJIAR LOCATION: INVESTIGATION: INVESTIGATION: TO OTHER CALCI: SIBLILARIY: TO OTHER CALCI: X05921; G1548; A30063; A30063; A30063; A30063; C CHANNEL; TRANSMEMBRANE; IUM CHANNEL; GLYCOPROTEIN; TAT 38 337 I AT 786 1068 I 1AT 786 1068 I 1AT 1105 1384 I 15MEM 52 70 SISMEM 89 108 S	FROM N.A.  87258269.  1., TAKESHIMA H., MIF KK., KOJIMA M., MATSU 128:313-318 (1987).  1. FROM N.A.  FROM N.A.  FROM N.A.  FROM N.A.  1. CAMPBELL K.P., M M.M.;  1. CAMPBELL K.P., M M.M.;  241:1661-1664 (1988).  171. CALCIUM CHANNE 171. THE L-TYPE CALC	STANDARD; L. 07, CREATED L. 07, LAST SE L. 27, LAST AN E-SENSITIVE L- ICULUS (RABBIT ZOA; CHORDATA; ORPHA.	42.13 rvative khvvqc :   RPSHSC	407 1471 1523 1738 1738 AA; 210096
N AND GAMMA.  INTEGRAL MEMBRANE PROTEIN. GELETAL MUSCLE. ZALCIUM CHANNEL ALPHA SUBUNITS. ZALCI	ENCE FROM N.A.  UE-SKELETAL MUSCLE;  LINE; 87258269.  BE T., TAKESHIMA H., MIKAMI A., FLOCKERZI V., TAKAHASHI H.,  AMANA K., KOJIMA M., MATSUO H., HIROSE T., NUMA S.;  RE 328:313-318 (1987).  RE 328:313-318 (1987).  ENCE FROM N.A.  UE-SKELETAL MUSCLE;  LINE; 88336904.  S.B., WILLIAMS M.E., WAYS N.R., BRENNER R., SHARP A.H.,  S.S., WILLIAMS M.E., MCKENNA E., KOCH W.J., HUI A., SCHWARTZ A.,  OLD M.M.;  FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING. THE ALPHA-1 SUBUNIT BINDS EXCITATIONE (DHP). A CALCIUM CHANNEL BLOCKER.  SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:	D; PRT; 1873 AA. CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE) TIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL (RABBIT). (RABBIT).	; Pred. No. 1.49e+00; 4; Mismatches 7; In 936	PHOSPHORYLATION (BY CAPK) (POTENTIAL). PHOSPHORYLATION (BY CAPK) (POTENTIAL). PHOSPHORYLATION (BY CAPK) (POTENTIAL). (POTE

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DT 07

SEQUENCE FROM N.A.

EUKARYOTA;

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.

YBR291C OR YBR2039.

YBBE\_YEAST STANDARD; PRT; 299 AA. 2381.52; 01-0CT-1994 (REL. 30, CREATED) 01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) PUTATIVE MITOCHONDRIAL CARRIER YER291C.

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1033 lrplrainrakglkhvvqc 1051

2 LRPFKALVREKGHRPSHSC 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHANNEL;
               Similarity
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80
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263
301
411
555
589
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646
684
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931
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998
1024
11062
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Conservative
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                                                                          1418
1469
              39.7%;
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786
1199
                                                             242783
               Score 60; DB 2; 1
Pred. No. 1.49e+00;
                                                           MW; 4FC5E64A CRC32;
                                                                                                                                                                                                                IV. $1 00 $2 00 $1 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2 00 $2
                                                                        POTENTIAL.
                                                                                         POTENTIAL.
                                                                                                                       POTENTIAL
                                                                                                                                       POTENTIAL
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                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ION TRANSPORT; VOLTAGE-GATED CHANNEL; DUPLICATION; PHOSPHORYLATION.
 Mismatches
                                                                                                                                                                                                                REPEAT II.
REPEAT II.
REPEAT II.
REPEAT II.
REPEAT II.
REPEAT II.
REPEAT III.
REPEAT IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                           Length 2171;
 Indels
0;
Gaps
0
```

MEDLINE; 94378722.
HOLMSTROEM K., BRANDT T.,
YEAST 10:547-562(1994).

KALLESOE T.;

STRAIN=S288C

Mar 24 11:16

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뭐
                            Query Match
Best Local Similarity
                                                   SEQUENCE
                                                                                            EMBL; L03521; G152354; -. PIR; S15295; S15295.
151 lrrlhglgreaghqp 165
                                                          DOMAIN
                                                                 DOMAIN
                                                                         DOMAIN
                                                                              CHAPERONE;
                                                                                  PROSITE; PS00636; DNAJ_NTER.
                                                                                                               . MICROBIOL. 5:737-745(1991).
SIMILARITY: TO PROKARYOTIC DWAJ, AND TO EUKARYOTIC DWAJ-LIKE
                                                                                                            PROTEINS.
                      8.
                                                         ; NODULATION.

2 71

76 93
96 121
                                                  392 AA;
                      Conservative
                            39.1%;
                                                 43565 MW;
                            Score 59; DB 6; L
Pred. No. 2.30e+00;
                                                               DNAJ-LIKE. GLY-RICH.
                     Ç.
                                                         ARG-RICH
                                                 CCD3D880 CRC32;
                     Mismatches
                     4;
                                  Length 392;
                     Indels
                     ٥,
                     Gaps
                   9
```

망 Best Matches Query Match 01-AUG-1992 01-AUG-1992 01-NOV-1995 NOLC\_RHIFR P26508; PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI; NOLC PROTEIN RHIZOBIUM FREDII EMBL; X76053; G429137; -. EMBL; Z36160; G536746; -. SEQUENCE TRANSMEM HYPOTHETICAL PROTEIN; MITOCHONDRION; INNER MEMBRANE; REPEAT; PROSITE; PS00215; MITOCH\_CARRIER. PIR; S44554; S44554. PIR; S39148; S39148. -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. INNER MEMBRANE (POTENTIAL).
-!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL 156 vrnysslvrdkg 167 TRANSMEM RANSMEM PRANSMEM TRANSMEMBRANE; Local 2 LRPFKALVREKG 13 39.1%; Similarity 50.0%; 6; 299 AA; (REL. Conservative 16 66 TRANSPORT. STANDARD; 23, CREATED)
23, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE) 36 P 86 P 133 P 235 P 32173 MW; Score 59; DB 10; Pred. No. 2.30e+00; POTENTIAL. 1; 01FF9E27 POTENTIAL. POTENTIAL. 4: PRT; POTENTIAL. Mismatches 392 CRC32; A 2; Length 299; Indels <u>.</u> Gaps 0

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RHIZOBIACEAE

STRAIN=USDA257; SEQUENCE FROM N.A. KRISHNAN H.B., PUEPPKE S.G.; MEDLINE; 91260457.

US-08-644-289-1.rsp

 $\overline{\sim}$ 

N LRPFKALVREKGHRP 16

Q

G11A OR: P47997; 01-FEB-1996 ORYSA (REL. 33, STANDARD; CREATED) PRT; 531 Ä

01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PROTEIN KINASE GIIA (EC 2.7.1.-) (FRAGMENT).

ORYZA SATIVA (RICE). EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE; STRAIN=CV. CYPERALES; GRAMINEAE. SEQUENCE FROM N.A. IR36; TISSUE=LEAF;

LAWTON M.A., YAMAMOTO R.T., HANKS S.K., LAMB C.J.;
PROC. NATL. ACAD. SCI. U.S.A. 86:3140-3144(1989).
-!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF METABOLISM AND -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS EMBL; J04556; G169788; -MEDLINE; 89240692. PROTEIN KINASES. STRONG, TO P.VULGARIS PVPK-1 SIGNAL TRANSDUCTION PROCESSES OF SER/THR-

BINDING ACT\_SITE DOMAIN NON\_TER SEQUENCE NP BIND DOMAIN NON TER TRANSFERASE; 531 AA; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING 480 156 171 267 339 58647 MW; PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

CYS-RICH INSERT. FAF6904A CRC32;

Query Match Best Local S Matches 268 lkpenvlvredgh 2 LRPFKALVREKGH Similarity 8 Conservative 14 280 38.4%; Pred. No. 3.53e+00; Score 58; DB 3; 2; Mismatches ښ. Length 531; Indels 0 Gaps <u>,</u>

Ş В

HAYASHIDA N., MIZOGUCHI T., YAMAGUCHI-SHINOZAKI K., SHINOZAKI K., GENE 121:325-330(1992).

-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN ROOT TISSUE WITH LOWER LEVELS FOUND IN LEAF, STEM, SEED AND FLOWER.

-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PK7 (EC 2.7.1.-). Q059<del>9</del>9; ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSP KPK7 MEDLINE; 93077048. SEQUENCE FROM N.A. CAPPARALES; CRUCIFERAE. 13 ARATH STANDARD; PRT; ANGIOSPERMAE; DICOTYLEDONEAE; 578 A

EMBL; S50281; -; NOT\_ANNOTATED\_CDS.

PROTEIN KINASES.

Mar 24 11:16

PIR; JC1385; JC1385.

PROSITE; PS00107; PROTEIN KINASE ATP.
PROSITE; PS00108; PROTEIN KINASE ST.
PROSITE; PS50011; PROTEIN KINASE DOM.
TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING.

DOMAIN

516

Mar 24 11.16

K

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RESULT
ID KG
AC PI
DT 01
DT 01
DT 01
DT 01
DT 02
DT 02
DT 05
DT 05
DT 05
DT 05
DT 06
DT 06
DT 07
           RESULT
ID PC
AC P2
DT 01
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                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                          Query Match 38.4%;
Best Local Similarity 61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
POL SFV3L STANDARD;
P27401;
01-AUG-1992 (REL. 23, CREATED)
                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
BINDING
ACT_SITE
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPK1 PHAVU STANDARD; PRT; 609 AA. P15792; 01-APR-1990 (REL. 14, CREATED) 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE) 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) PROTEIN KINASE PYPK-1 (EC. 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00108; PROTEIN KINASE ST.
PROSITE; PS50011; PROTEIN KINASE DOM.
TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAWTON M.A., YAMAMOTO R.T., HANKS S.K., LAMB C.J.;
PROC. NATL. ACAD. SCI. U.S.A. 86:3140-3144(1989).
-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. STRONG, TO RICE GIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J04555; G169361; -. PIR; A30311; A30311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00107; PROTEIN_KINASE_ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P05132; 1CTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89240692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
                                                                                                                                                                                                    355 lkpenvlvredgh 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FABACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 lkpenvlvredgh 320
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2 LRPFKALVREKGH 14
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                                                                                                                                                                                                                                                                                                                                                                               400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182
188
211
307
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                             565
243
258
258
354
421
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211
307
                                                                                                                                                                                                                                                                                                                                                      68101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64286 MW;
                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                        Score 58; DB 5; Length 609; Pred. No. 3.53e+00;
                                                                                                                                                                                                                                                                                                                                                                                             ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58;
                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                          CYS-RICH INSERT.
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ?
                                                                                                                                                                                                                                                                                                                                               A7E5A35F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9DB8E278 CRC32;
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 3.53e+00;
                                                         1157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ω</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 578;
                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Search completed: Mon Mar 24 11:18:42 1997 Job time: 11 secs.

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Q
                                В
                                                                                                                           Matches
                                                                        Query Match 38.4%;
Best Local Similarity 44.4%;
                                                                                                                        ENDONUCLEASE; POLYPROTEIN.
ACT_SITE 38 38
SEQUENCE 1157 AA; 13122
                                                                                                                                                                                                                             MEDLINE; 92124734.

RENNE R., FRIEDL E., SCHWEIZER M., FLEPS U., TUREK R.,

NEUMANN-HAEFELIN D.;

VIROLOGY 186:597-608(1992).

-!- PIM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

-!- THIS POLYPROTEIN IS PROBABLY SYNTHESIZED AS A GAG-POL POLYPROTEIN
                                                                                                                                                                 HYDROLASE; ASPARTYL PROTEASE; RNA-DIRECTED DNA POLYMERASE;
                                                                                                                                                                                                   EMBL; M74895; G334872; -.
                                                                                                                                                                                       PIR; B40820; GNLJLK.
                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
POL POLYPROTEIN (CONTAINS: PROTEASE (EC 3.4.23.-);
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE).
                          726 lkpdiiiihekghqptas 743
                                                                                                                                                                                                                                                                                                                                                                    SPUMAVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                            VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                              SIMIAN FOAMY VIRUS (TYPE 3 / STRAIN LK3) (SFV-3).
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
 2 LRPFKALVREKGHRPSHS 19
                                                                                                                                                                                                                       BY A +1 FRAMESHIFT.
                                                            8
                                                         Conservative
                                                                                                                        131225 MW;
                                                                        Score 58; DB 7; I
Pred. No. 3.53e+00;
                                                         6; Mismatches
                                                                                                                                        BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-644-289-1<sub>.75</sub>p
                                                                                                                      C1425458 CRC32;
                                                         4; Indels
                                                                                       Length 1157;
                                                                                                                                                                                                                                                                                                                                                                                                                                            REVERSE
                                                        0;
                                                      Gaps
                                                        <u>,</u>
```

Mar 24 11:16

(MT)

Release 2.1D John F. Coilins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 24 11:18:02 1997; MasPar time 2.66 Seconds 193.564 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: 1 SLRPFKALVREKGHRPSHSC 20 (1-20) from US08644289.pep 151 >US-08-644-289-1

Scoring table: PAM 150 Gap 15

82182 seqs, 25727515 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc 14:unrev

Statistics: Mean 27.793; Variance 45.751; scale 0.607

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Length DB	1	ID	Description	Pred. No
μ.	65	43.0	245	14	S54125	pVIII protein - Avia	1.44e+00
2	64	42.4	1166	œ	A39432		2.08e+00
ω	62	41.1	164	12	S14016	X16 protein - mouse	4.32e+00
.4	62	41.1	1873	12	A55645	voltage-dependent ca	4.32e+00
5	60	39.7	116	S		T-cell receptor beta	8.83e+0
6	60	39.7	247	_		cytotoxic T-lymphocy	8.83e+0
7	60	39.7	347	12		calcium channel prot	8.83e+00
80	60	39.7	466	و	A54125	ferrochelatase (EC 4	8.83e+00
9	60	39.7	1331	12	S05011	calcium channel alph	8.83e+00
10	60	39.7	1610	12	A46227	voltage-dependent Ca	8.83e+0
::	60	39.7	1646	12	JH0422	voltage-dependent ca	8.83e+00
12	60	39.7	1687	\$			0 00 - 0

385

### ALI GNMENTS

Db 145 rplvrgi ::    : Qy 6 KALVREE	Query Match 43.0%; Best Local Similarity 40.0%; Matches 6; Conservative	##status ##residues ##cross-re: SUMMARY	#accession	#submission #description	#authors	ACCESSIONS REFERENCE	ORGANISM DATE	RESULT 1 ENTRY
145 rplvrgrsrrpprwc 159 ::    :::  ::  6 KALVREKGHRPSHSC 20	43.0%; Score 65; DB 14; Length 245; imilarity 40.0%; Pred. No. 1.44e+00; 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;	##status preliminary ##residues 1-245 ##label HES ##cross-references EMBL:x84724 Y #length 245 #molecular-weight 26877 #checksum 1107	and organisation of the genome. S54125	submitted to the EMBL Data Library, February 1995 The sequence of the two fibers of an avian adenovirus (CELO)	Hess, M.; Cuzange, A.; Chroboczeck, J.; Ruigrok, R.; Jacrot, B.	\$54125 \$54125	#formal name Avian adenovirus 08-Jul-1995 #sequence_revision 08-Jul-1995 #text_change 08-Jul-1995	\$54125  #type complete

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                                                                            Query Match 41.1%;
Best Local Similarity 50.0%;
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Best Local Similarity 69.2%;
Matches 9; Conservative
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                               137 rslsrernhkpsrs 150
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                                                                                                                                                                                                             ##residues
                                                                                                                                                                                                                        ##molecule_type mRNA
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   KALVREKGHRPSHS
                                                                                                                                                                        #superfamily ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                   A differentially expressed murine RNA encoding a protein with
                                                                                                                            #length 164
                                                                                                                                                                                                                                             514016
                                                                                                                                                                                                                                                                                                     Ayane, M.; Preuss, U.; Koehler, G.; Nielsen, Nucleic Acids Res. (1991) 19:1273-1278
                                                                                                                                                                                                                                                                                                                                                           S14016
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J. Bacteriol. (1991) 173:3644-3655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal name Bacillus subtilis
21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                 #length 1166  #molecular-weight 134630  #checksum 5494
                                                                Conservative
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                                                                                                                                                                                                            1-164 ##label AYA
                                                                                                                         #domain ribonucleoprotein repeat homology #label
pth 164  #molecular-weight 19329  #checksum 8302
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                                                                            Score 62; DB 12;
Pred. No. 4.32e+00;
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    Mismatches

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Best Local Similarity 53.8%;
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Best Local Similarity 42.1%;
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#map_position 1q31-q32
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                    12 likekgqrvnmsc 24
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LVREKGHRPSHSC 20
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                                                                                                                                           the sequence was determined from the differentiated gene superfamily immunoglobulin V region; immunoglobulin homology length 116 schecksum 1551
                                                                                                                                                                                                                                                            E30563
                                                                                                                                                                                                                                                                                                             T cell receptor beta-chain genes in the rat. Availability and pattern of utilization of V gene segments differs from that
                                                                                                                                                                                                                                                                                                                                                                                                               E30563
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                                                                                                                                                                                                                                                                                                                                                                                                                                       #formal_name Rattus norvegicus #common_name Norway rat
03-Apr-1989 #text_change
                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hogan, K.; Powers, P.A.; Gregg, Genomics (1994) 24:608-609
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24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
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                                                                                       Score 60; DB 5; Length 116; Pred. No. 8.83e+00;
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Pred. No. 4.32e+00;
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CLASSIFICATION KEYWORDS FEATURE GENETICS COMMENT REFERENCE REFERENCE REFERENCE ACCESSIONS ORGANISM ALTERNATE\_NAMES Query Match Best Local Similarity 1-18 19-20 49-65, 142-209, 173-188 64, 108, 203 21-240 21-247 #introns #map\_position 14 lymphocyte-specific serine proteases CCPI and CCPII. #cross-references MUID:89062424 #authors # journal #authors lymphocyte-specific genes. #cross-references MUID:86208120 # journal #authors accession accession | journal #accession contents cross-references MUID:86284960 ##molecule\_type DNA ##residues 1-247 ##label LO2 ##cross-references EMBL:X04072 ##cross-references GB:M22526 ##residues ##molecule\_type mRNA ##cross-references GB:M12302 ##molecule\_type mRNA
#fresidues 1-247 ##label LOB This enzyme is probably necessary for target cell lysis cell-mediated immune responses. #superfamily trypsin; trypsin homology Lobe, C.G.; Upton, C.; Duggan, B.; Ehrman, N.; Letellier, Bell, J.; McFadden, G.; Bleackley, R.C. Biochemistry (1988) 27:6941-6946
Organization of two genes encoding cytotoxic T #length 247 #molecular-weight 27470 #checksum hydrolase; serine proteinase; T-cell 19/1; 68/2; 113/3; 200/3 A28952 A93382 A90536 chromosome mapping Brunet, J.F.; Dosseto, M.; Denizot, F.; Mattei, M.G.; Clark, Nature (1986) 322:268-271 A94288 A93382 Novel serine proteases encoded by two Science (1986) 232:858-861 CPPI; cytotoxic cell protease 1; cytotoxic T-cell-specific The inducible cytotoxic T~lymphocyte-associated gene Lobe, C.G.; Finlay, B.B.; Paranchych, W.; Paetkau, V.H.; A94288 A94288; A93382; A28952; A00956 #formal\_name Mus musculus #common\_name house mouse
04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change cytotoxic T-lymphocyte proteinase (EC 3.4.21.-) 1 precursor -W.R.; Haqqi, T.M.; Ferrier, P.; Nabholz, M.; Schmitt-Verhulst, A.M.; Luciani, M.F.; Golstein, P. chromosome 14. Bleackley, R.C. transcript CTLA-1 sequence and gene localization to mouse 14-Jul-1994 factive\_site His, Asp, Ser #status predicted 1-247 ##label BRU #domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label APT\
#product cytotoxic T-lymphocyte proteinase 1 #status
predicted #label MPT\ #disulfide\_bonds #status predicted\ domain trypsin homology #label TRY 39.7%; Score 60; DB 1; I Pred. No. 8.83e+00; DB 1; Length 247; cytotoxic T 92 'n

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                Query Match 39.7%;
Best Local Similarity 43.8%;
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Best Local Similarity 42.1%;
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# #length 347 #molecular-weight 40393 #checksum
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                                                                  chloroplast; .
#length 466 ;
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                                                                                                                                                                                             Isolation of a cDNA encoding chloroplast ferrochelatase from Arabidopsis thaliana by functional complementation of a
                                                                                                                                                                                                                                    J. Biol. Chem.
                                                                                                                                                                                                                                                                                                     A54125
                                                                                                                                                                                                                                                                                                                             07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                              #formal_name Arabidopsis thaliana #common_name mouse-ear
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   Conservative
                                                                                                                                                                                                                                                                 Smith, A.G.; Santana, M.A.; Wallace-Cook, A.D.M.; Roper,
                                                                                                                                                                                                                                                                                                                                                                                             A54125 #type complete ferrochelatase (EC 4.99.1.1) precursor, chloroplast
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                                                                                                                     1-466 ##label SM1
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                                                                  #molecular-weight 52032 #checksum
                                                                                                                                                                                                                                  (1994) 269:13405-13413
               Score 60; DB 9; I
Pred. No. 8.83e+00;
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##experimental_source insulin-secreting cell line HIT-T15
##note sequence extracted from NCBI backbone
Y #length 1610 #molecular-weight 182326 #checksum 806
                                                                    ##cross-references NCBIP:123692
                                                                                                                  #molecule_type mRNA
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Local Similarity 42.1%;
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                                                                                                                                                                                                                           Cloning of a novel alpha 1-subunit of the voltage-dependent
                                                                                                                                                                                                                                                  Yaney, G.C.; Wheeler, M.B.; Wei, X.; Perez-Reyes, E.;
Birnbaumer, L.; Boyd III, A.E.; Moss, L.G.
Mol. Endocrinol. (1992) 6:2143-2152
                                                                                                                                                                                                                                                                                                                                                                                      #formal_name Mesocricetus auratus #common name golden hamster
27-Oct-1993 #sequence_revision 18-Nov-1994 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dihydropyridine receptor, cardiac; voltage-dependent calcium
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Pred. No. 8.83e+00;
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Ş 밁 SUMMARY FEATURE COMMENT KEYWORDS TITLE REFERENCE DATE ENTRY RESULT Ş B REFERENCE ACCESSIONS ORGANISM Query Match 39.7%; Best Local Similarity 42.1%; Query Match 39.7%; Best Local Similarity 42.1%; 464,848,1489,1584 #binding\_site phosphate (Ser) (covalent) #status Matches 154, 224, 328 #accession #title # journal #authors #accession #title # journal #authors 463-1491 cross-references MUID:90239020 #cross-references MUID:91299338 988 lrplrainrakglkhvvqc 1006 ##molecule\_type mRNA
##residues 1247-1434 ##label SNU ##status 987 lrplrainrakglkhvvqc 1005 \*\*experimental\_source brain ##molecule\_type mRNA ##experimental\_source brain #cross-references GB:M57682 ##residues 2 LRPFKALVREKGHRPSHSC 20 11 LRPFKALVREKGHRPSHSC Calcium channels are essential for many cellular functions, such as of electrical activity, and neurotransmitter regulation. muscle contraction, propagation of action potentials, maintenance 8 œ #length 1646 #molecular-weight 186842 #checksum Snutch, T.P.; Leonard, J.P.; Gilbert, M.M.; Lester, H.A.; glycoprotein D35901 Rat brain expresses a heterogeneous family of calcium Proc. Natl. Acad. Sci. U.S.A. (1990) 87:3391-3395 JH0422 A35901 Molecular cloning of multiple subtypes of a novel rat brain isoform of the alpha 1 subunit of the voltage-dependent #formal\_name Rattus norvegicus #common\_name Norway rat
31\_Mar\_1992 #sequence\_revision 31\_Mar\_1992 #text\_change Conservative Neuron (1991) 7:35-44 Hui, A.; Ellinor, P.T.; Krizanova, O.; Wang, J.J.; Diebold, JH0422 JH0422; D35901 voltage-dependent calcium channel complex alpha-1 chain - rat Davidson, N. Conservative calcium channel. R.J.; Schwartz, 08-Feb-1996 the nucleotide sequence is not given #binding\_site carbohydrate (Asn) (covalent) #status preliminary; not compared with conceptual translation 1-1646 ##label HUI #domain calcium-binding #status predicted #label EFC predicted predicted\ #type complete 20 Score 60; Pred. No. 8.83e+00; Score 60; DB 12; Length 1610; Pred. No. 8.83e+00; 4; Mismatches 7; Indels 4; Mismatches DB 12; Length 1646; Indels <u>,</u>, <u>,</u> 699 Gaps Gaps 0 0

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                        #formal name Mus musculus #common name house mouse
31_Dec-1993 #sequence_revision 31_Dec-1993 #text_change
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                                                                          A44467 #type complete complex alpha-1 chain mbC
                                                                                                                                                                                                                                                                                                                                                             A30063
                                                                                                                                                                                                                                                                                                                                                                                        Primary structure of the receptor for calcium channel blockers from skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                          Nature (1987) 328:313-318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanabe, T.; Takeshima, H.; Mikami, A.; Flockerzi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **experimental_source brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
##residues 1-2139 ##label MA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LRPFKALVREKGHRPSHSC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
            te the nucleotide sequence is not given Calcium channels are essential for many cellular functions, such as muscle contraction, propagation of action potentials, maintenance of electrical activity, and neurotransmitter regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                                                                                           Davidson, N.

Proc. Natl. Acad. Sci. U.S.A. (1990) 87:3391-3395
                                                                                                                                                                                                                            Rat brain expresses a heterogeneous family of calcium
                                                                                                                                                                                                                                                                                                  Snutch, T.P.; Leonard,
                                                                                                                                                                         C35901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Distinct calcium channels are generated by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Snutch, T.P.; Tomlinson, W.J.; Leonard, J.P.; Gilbert, M.M. Neuron (1991) 7:45-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JH0426; C35901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #formal_name Rattus norvegicus #common_name Norway rat
31_Mar_1992 #sequence_revision 31-Mar-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JH0426 #type complete voltage-dependent calcium channel complex alpha-1 chain rbC-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein
#length 2139 #molecular-weight 240136 #checksum 8452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A44467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ma, W.J.; Holz, R.W.; Uhler, M.D.
J. Biol. Chem. (1992) 267:22728-22732
Expression of a cDNA for a neuronal calcium channel alpha I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A44467
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                                                                                                                                                                                                                    channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splicing and are differentially expressed in the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-Feb-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subunit enhances secretion from adrenal chromaffin cells
                                                                                                  1139-1384 ##label SN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-2140 ##label SNU
                                                                                                                                            preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                       the codon for 1758-Tyr is TAA; the authors claim that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence extracted from NCBI backbone
                                                                                                                                                                                                                                                                                                                                              clone contains TAC at this position
                                                                                                                                                                                                                                                                                                                                                              this is an artifact of the cDNA cloning. Another cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score bu, Pred. No. 8.83e+00;
                                                                                                                                                                                                                                                                                                J.P.; Gilbert, M.M.; Lester,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 2139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                  H.A.;
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1545, 1597, 1670,

SUMMARY Mar 24 11:16 1818, 1898 #binding\_site phosphate (Ser) (covalent) #status
predicted
#length 2140 #molecular-weight 240188 #checksum 1204 US-08-644-289-1 rpr

=

Query Match 39.7%; Score 60; DB 12; Length 2140; Best Local Similarity 42.1%; Pred. No. 8.83e+00; Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Db 1003 lrplrainrakglkhvvqc 1021 |||::|: | ||: | 0y 2 LRPFKALVREXGHRPSHSC 20

Search completed: Mon Mar 24 11:18:15 1997 Job time : 13 secs.

\*

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:41:07 1997; MasPar time 58.62 Seconds 533.919 Million cell updates/sec

Tabular output not generated.

Perfect Score: Description: Title: 38 (1-38) from US08644289.seq >US-08-644-289-2

N.A. Sequence: Comp: 1 AGTCAGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38 TCAGTCCGGAATCTCAATTTCCTACGGGTACGATGTCT

Scoring table: TABLE default Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database: 1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PIN 9:PRI 10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7 23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5 30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2 37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2 44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1 51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8 58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1 64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8 71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4 78:VRL5 79:VRL6 80:VRL7 81:VRL8 genbank 94

Database: genbank-new5

82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG 89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL u-embl46\_94

Database:

Statistics: Mean 7.583; Variance 2.828; scale 2.681

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mar 25 02:40 US-08-644-289-2.rge

SUMMARIES

5.41e+00 5.41e+00	Rat s-myc protein gen Mouse XRCC1 DNA repai	RATMYCS MUSXRCC1G	8019 69 37349 68	44.7	17	c 44 45
	Bacteriophage phi-X17	PHIX174	5386 41	44.7	17	
5.41e+00	Cat mRNA for p53 prot	CATP53A		44.7	17	c 40
1.08e+00	CAS-BR-E murine leuke	CASBREML		47.4	18	c 39
•	sus monkey	MACP53A		50.0	19	37
2.04e-01	lymph node mRNA	CATP53		50.0	19	36
2.04e-01	Cat lymph node mRNA f	CATP53		50.0	19	33 G
2.04e-01	an mRNA	HSP53R	2066 54	50.0	19	33
2.04e-01	4.	HUMP53T		50.0		32
2.04e-01	ın Green	CAP53		50.0	19	ω 21
2.046-01	Human pos cellular tu	HSD53	1317 54	50.0	19	30
2.04e-01	p53 cellular	HUMTP53B		50.0	19	28
2.04e-01	mRNA for	HSP53005	1179 54	50.0	19	27
2.04e-01	mRNA for	HSP53004		50.0	19	26
04e-	mRNA for	HSP53007		50.0	19	25
2.04e-01	Human mRNA for mutate	HSP53003	1179 54	50.0	19	24
04e-0	mRNA for	HSP53009		50.0	10	22
	mRNA for	HSP53008		50.0	19	21
04e-	mRNA for	HSP53011		50.0	19	20
2.04e-01	mRNA for mutat	HSP53002		50.0	19	19
6		HSP53006		50.0	19	18
.04e-0	Human phosphoprotein	HUMP53A10	136 60	50.0	19	17
2 04e-01	Human cellular phosph	HIMPS310		50.0	10	16
. 666-0		RAIRSEUDO		53.6	2 0	 
	norvegicus	RNP SUEDO	1447 12	52.6	20	13
.51e-0	Rat mRNA for nuclear	RNP53		63.2	24	12
.51e-0	norvegicus	RNU07019		Ψ	24	11
.51e-	vo .	RATP53TS07		Ψ	24	10
4.20e-14	Mouse pseudogene for	MMP53P	2132 64	89.5	34	و م
P	mKNA for cell	MAE OUR		۰.	ر 14 د	o ~
.28e-		MUSP53M	1772 67	9.9	ى 4.	J 65
.28e-	for t	MMP 53	-	. 9	34	. <sub>.</sub> .
.28e-	p53 mRNA,	MUSP53C		9	34	4
4.28e-14	p53 mRNA,	MUSP53A		9	34	ω
8e-	p53 mRNA,	MUSP53B		9.	34	2
4.28e-14	Murine gene for cellu	MMANT10	107 63	89.5	34	1
Pred. No.	Description	ID	Length DB	Match 1	Score	No.
				3		D 1+

# ALI GNMENTS

ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION	DEFINITION	LOCUS	RESULT 1
Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	house mouse.	antigen.	g49989	X00884	Murine gene for cellular tumour antigen p53 (exon 10).	MMANT10 107 bp DNA ROD 16-JUN-1995	

MEDLINE REFERENCE

85027173

(bases 1 to 107)

JOURNAL

EMBO J. 3 (9), 2179-2183 (1984)

TITLE

A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306 (5943), 594-597 (1983)

Lavie, V., Hazum, S. and Givol, D.

AUTHORS

Zakut-Houri, R., Oren, M., Bienz, B.,

FEATURES

source

1..107

Location/Qualifiers

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5 AGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38

/organism="Mus musculus"

exon

MEDLINE

84068204

JOURNAL

REFERENCE AUTHORS

Muridae; Murinae;

Mus.

(bases 1 to 107)

TITLE

Analysis of the gene coding for the murine cellular Bienz, B., Zakut-Houri, R., Givol, D. and Oren, M.

tumour antigen

Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha;

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SOURCE
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                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse p53 mRNA, complete cds, clone p53-m11.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Animalia; Chordata;
                                                                                                                                                                                                                                                                        87064640
                                                                                                                                                                                                                                                                                                                                               Rotter, V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse (BALB/c) Meth A library, cDNA to mRNA, clone p53-m11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53 gene.
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                                                                                                                                                                                                                                                                                         Mol. Cell. Biol. 6,
                                                                                                                                                                                                                                                                                                           splicing
                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Rodentia; Myomorpha;
                                                                                                                                                                                                                                                                                                                           Immunologically distinct p53 molecules generated by alternative
                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1241)
               /db_xref="PID:g200201"
/translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL
LLPQDVEEFFEGPSEALRVSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQKTYQG
                                                                                                                                          /sequenced_mol="cDNA to mRNA"
/tissue_lib="Meth A"
NYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMA I Y
                                                                                    /map="11"
                                                                                                     /gene="p53"
                                                                                                                           69..1241
                                                                                                                                                                              /sub_species="domesticus"
                                                                                                                                                                                                 /strain="BALB/c"
                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                     /codon_start=1
                                                                                                                                                                                                                                      1..1241
                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                              Yokota, K., Wolf, D., Brill, E., Shohat, O. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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4

ORIGIN BASE COUNT 289 മ FEMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD" RDRRTEEENFRKKEVLCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTLKIRGRKR PPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPG KKSQHMTGVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE 376 c 321 g 255 t

밁 Matches Query Match 89.5%; Best Local Similarity 100.0%; 1096 aggccttagagttaaaggatgcccatgctacaga 1129 34; Conservative Score 34; DB 67; Pred. No. 4.28e-14; 0; Mismatches <u>,</u> Length 1241; Indels <u>,</u> Gaps

0

NID KEYWORDS ACCESSION DEFINITION TOCOS SOURCE RESULT ORGANISM ω M13872 Mouse p53 mRNA, Mus musculus Eutheria; Rodentia; Myomorpha; Muridae; Murinae. 1 (bases 1 to 1285) Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; pcD-p53. Mouse (BALB/c) nontransformed helper T-cell, cDNA to mRNA, clone p53 gene g200198 MUSP53A 1285 bp complete cds, clone pcD53. mRNA 05-NOV-1992

ORIGIN

BASE COUNT

27

a)

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20 t

/label=ex10

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Matches

Conservative

Query Match 89.5%; Best Local Similarity 100.0%;

Score 34; DB 63; Pred. No. 4.28e-14;

Length 107;

0; Mismatches

0;

Indels

<u>,,</u>

Gaps

0

FEATURES REFERENCE TITLE MEDLINE JOURNAL AUTHORS Arai, N., Nomura, D., Yokota, K., Wolf, D., Brill, E., Shohat, O. 87064640 Immunologically distinct p53 molecules Rotter, V. splicing Cell. Biol. 6, 3232-3239 (1986) Location/Qualifiers generated by alternative

CDS source /sub\_species="domesticus"
/cell\_type="nontransformed helper T-cell" 113..1285 /sequenced\_mol="cDNA to mRNA" /strain="BALB/c" /codon\_start=1 organism="Mus musculus"/

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                Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
                                       Mus musculus
                                                       house mouse.
                                                                                                                                Mouse mRNA for transformation associated protein p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             different tissue types
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUSP53C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunologically distinct p53 molecules generated by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L12, cDNA to mRNA,
                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                        Conservative
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 Eumetazoa; Bilateria;
                                                                                                                                                                                                                                                                                                                                                                                                                       FEMFRELNEALELKDAHATEESGDSRAHSSLQPRAFQALIKEESPNC*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="PID:g200203"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Ab-MuLV transformed Meth A fibroblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_line="normal T-cell line L12"
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Pred. No.
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Coelomata; Deuterostomia;
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 Chordata;
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LOCUS DEFINITION ij RESULT Ş В ORIGIN COMMENT REFERENCE BASE COUNT FEATURES REFERENCE SOURCE ACCESSION REFERENCE EYWORDS AUTHORS TITLE TITLE AUTHORS TITLE ORGANISM Matches Query Match 89.5%; Best Local Similarity 100.0%; MEDLINE JOURNAL AUTHORS MEDLINE JOURNAL JOURNAL 1147 aggccttagagttaaaggatgcccatgctacaga 1180 CDS source 5 AGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38 Mouse p53 cellular tumor antigen, mRNA. K01700 Jenkins, J.R., Rudge, K., Redmond, S. and Wade-Evans, A. Cloning and expression analysis of full length mouse encoding the transformation associated protein p53 Nucleic Acids Res. 12 (14), 5609-5626 (1984) Pennica, D., Goeddel, D.V., Hayflick, J.S., Reich, N.C., Anderson, C.W. and Levine, A.J. products and the adenovirus Ela proteins. All three of these proteins are rich in proline, contain proline runs or clusters, and are localized in the nucleus of tranformed cells. The Ela proteins and p53 have been shown to have very short half-lives [2]. The The amino acid sequence of murine p53 determined from a cDNA clone Virology 134, 477-482 (1984) A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306, 594-597 (1983) Mus musculus Mouse embryo F9 carcinoma cells, cDNA p422, p208 [1], and clone pp53-1 [2]. sequence of cDNA in [1] was established The murine p53 protein is similar to the avian and human myc gene 86072076 84068204 Zakut-Houri, R., Oren, M., Bienz, B., Eutheria; Rodentia; Myomorpha; Muridae; Murinae. Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; DNA-binding protein; antigen; p53 gene; tumor antigen g200204 Data kindly reviewed (19-FEB-1986) by A. Wade-Evans 84272240 Sciurognathi; Myomorpha; Muridae; Murinae; Mus. 1 (bases 1 to 1377) Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; (bases 105 to 1772) (bases 1 to 1716) 316 Conservative 306, ø /codon\_start=1
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/tanslation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL/translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSSPHCMDDLLLPRDVEEFFEGPSEALRVSGAPAAQDPVTETPGQWPAPAPWPDLSSFVPSGKTYQGN EMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD\* DRRTEEENFRKKEVLCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTLKIRGRKRF PEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGR KSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYEP YGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYK /note="p53" /organism="Mus musculus" 23..1292 1..1377 ocation/Qualifiers 422 c 1772 bp Score 34; DB 64; Pred. No. 4.28e-14; 0; 348 g Mismatches 291 t cDNA to Lavie, V., Hazum, S. and Givol, D. 0; Length 1377; δ ROD mRNA, analysing Indels clones Glires; Rodentia; 03-MAY-1985 <u>,</u> p176, cDNA sequences Gaps Choanata; separate p271, <u>,</u> and

FEATURES

relative to the cDNA [1].

Location/Qualifiers

source

/cell

CDS

/map="11" 158..1330

/gene="p53"

/map="11" /gene=" nRNA

/tissue\_type="carcinoma" <1..1668

/sequenced\_mol="cDNA to mRNA" /dev\_stage="embryo" organism="Mus musculus" line="F9"

cDNA clones; p176 (bp 1-1247), p271 (bp 69-638), p422 (bp 1288-1719), and p208 (bp 1432-1719) [1]. There is only one functional p53 gene in the mouse genome.

p422

sequence of the murine p53 psuedogene, also reported by [1] (see separate entry), and the cDNA sequence are almost identical from nucleotide 186 onward. Upstream of this position the two sequences

gene, mostly due to post-translational modifications [1]. The existing different forms of murine p53 must be products of the same

the two sequences differ by only 4%. The differences are due to

substitutions and to some small deletions or additions in this gene deverge totally and no homology can be observed; downstream of here

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Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol,D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306 (5943), 594-597 (1983)
                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                  MMP53R 1773 bp RNA ROD Mouse mRNA for cellular tumour antigen p53.
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
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bp upstream of NcoI site.
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Pred. No. 4.28e-14;
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Best Local Similarity 100.0%;
Matches 34; Conservative
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Analysis of the gene coding for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-NOV-1985) to the EMBL/GenBank/DDBJ databases
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NYGFHLGFLQSGTAKSVMCTYSPP LNKLFCQLVKTCPVQLWVSA TPP AGSRVRAMA I Y
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Pred. No. 4.28e-14;
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e murine cellular tumour antigen
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LLPQDVEEFFEGPSEALRVSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQKTYQG NYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIY

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/codon\_start=1 /product="cellular tumor antigen" /db\_xref="PID:g200205"

FEMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD." RDRRTEEENFRKKEVLCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTLKIRGRKR PPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPG KKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE

Ş 5 AGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38

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Mouse

p53 cellular tumour antigen psuedogene

MUSP53PG

2130 윻

DNA

ROD

03-MAY-1985

NID ACCESSION DEFINITION

g200206 K02110

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                                                                                                                                                                                                                                                                                                                                          AGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38
                                                                                                                                                                                                2132 bp DNA ROD
Mouse pseudogene for cellular tumour antigen p53.
X01225 K02110
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                                                                                                                                                                                 g53574
                                          Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     separate entry), and the psuedogene are almost identical from nucleotide 186 onward. Upstream of this position the two sequences deverge totally and no homology can be observed; downstream of here the two sequences differ by only 4%. The differences are due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol,D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306, 594-597 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen; p53 gene; processed pseudogene; tumor antigen. Mouse 3.3-kb fragment isolated from a BALB/c genomic library, clone
                                                                                                                                                            antigen; pseudogene; tumor antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84068204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Sciurognathi; Myomorpha; Muridae; Murinae; Mus
                                                                                                                  Mus musculus
                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relative to the cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substitutions and to some small deletions or additions in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    introns, and is bounded by direct repeats (bp 169-181 and bp 1852-1861), suggesting that it is a processed gene which resulted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The DNA sequence of pCh53-11 contains a long poly-A tract, lacks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Rodentia; Myomorpha; 1 (bases 1 to 2130)
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                       Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of the murine p53 cDNA, also reported by [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trom reverse transcription of the mature mRNA.
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Pred. No. 4.28e-14;
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Best Local Similarity 100.0%;
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Nature 306 (5943), 594-597 (198
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                                                                                                                                                                                                                                               93181268
                                                                                                                                                                                                                                                            Structure of the rat p53 tumor suppressor gene Nucleic Acids Res. 21, 713-717 (1993)
                                                                                                                                                                                                                                                                                          Hulla, J.E. and Schneider, R.P.Sr..
                                                                                                                                                                                                                                                                                                                        Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
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                                                                                                                                                                                                                                                                                                                                                                                               tumor suppressor.
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                                                                    /gene="p53"
                                                                                         27..133
                                                                                                      /number=8
                                                                                                                       /note="intron 8 is ~830 bp"
                                                                                                                                                                  /sequenced_mol="DNA"
                                                                                                                                                                                  /strain="Sprague-Dawley"
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                                                                                                                                    /gene="p53"
                                                                                                                                                                                                  organism="Rattus norvegicus"
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Best Local Similarity 85.3%; Matches 29; Conservative

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g460923

DEFINITION ACCESSION

Rattus norvegicus Wistar clone U07019

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1273 bp

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pR53P1 p53 pseudogene.

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-FEB-1994) Yue Lin, Department of Microbiology, National University of Singapore, Lower Kent Ridge Road, Singapore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and characterization of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin, Y. and Chan, S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                      National University of Singapore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muridae; Murinae; Rattus.
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359..539
        /gene="p53"
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120..358
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                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                         /strain="Wistar"
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note="corresponds
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                                                                                                                                                                       Submitted (26-SEP-1988) to the EMBL/GenBank/DDBJ databases. Soussi T., Universite Pierre et Marie Curie, Unite d'Oncologie Moleculaire, IRSC - CNRS, BP 08 94802 Villejuif, France
                                                                                                                                                                                                                                                                                                                                                                                   g56828
                                                                                                                                                                                                                                                                                                                                                                                                                              RNP53
                                                                                                                                Nucleotide sequence of a cDNA encoding the rat p53 nuclear
                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                     Norway rat.
                                                                                                                                                                                                                                                                                                                                                                  oncoprotein p53.
                                                                                                                                                                                                                                                                                                                                                                                                               Rat mRNA for nuclear oncoprotein p53
                                                                         Data kindly reviewed (09-Feb-1989)
                                                                                                   Nucleic Acids Res. 16 (23), 11384 (1988)
                                                                                                                     oncoprotein
                                                                                                                                               Soussi, T., Caron de Fromentel, C., Breugnot, C. and May, E.
                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                     Soussi,
                                                                                                                                                                                                                                                                 Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                          Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
                                                                                        89083585
                                                                                                                                                            (bases 1 to 1627)
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/organism="Rattus norvegicus"
/cell_line="Py T21"
24...1199
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1154..>1273
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641..750
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751..887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 70;
Pred. No. 2.51e-05;
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                                                                         by Soussi
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BASE COUNT
ORIGIN
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Best Local Similarity
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L12046;
16-MAR-1993 (Rel. 35, Created)
14-APR-1996 (Rel. 47, Last updated, Version 3)
Rattus norvegicus p53 (PG-III) pseudogene, partial ORF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
                                                                                                                       CDS
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1-1447
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                                                                                                                                                                                                           /note="this region of the pseudogene corresponds to exon 3 of the rat p53 cDNA; putative" 98...315\,
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GRDRRTEEENFRKKEEHCPELPPGSAKRALPTSTSSSPQQKKKPLDGEYFTLKIRGRE
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/note="tumor suppressor; this region of the pseudogene
                                                                                                                     of the rat p53 cDNA; putative" <168..>542
                                                                                                                                                                                                                                                                                                    76..97
                                                                                                                                                                                                                                                                                                                             /note="this site within the pseudogene corresponds to the ATG translation start site of the rat p53 cDNA; putative"
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potential open reading frame; putative; NCBI gi: 206473"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/strain="Fischer 344"
                                                                                                                                                                               /note="this region of the pseudogene corresponds to exon 4
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2.51e-05;
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exon

misc\_signal

/note="this region of the pseudogene of the rat p53 cDNA; putative" 2..4

corresponds to exon

/note="this site within the pseudogene corresponds to the ATG translation start site of the rat p53 cDNA; putative"

/note="this region of the pseudogene

corresponds to exon

BASE COUNT ORIGIN FEATURES COMMENT Best Loc Matches AUTHORS TITLE Query Match MEDLINE JOURNAL exon exon misc\_signal exon exon exon exon CDS exon exon misc\_signal exon source Local Cloning and sequence of a processed p53 pseudogene from rat: a potential source of false 'mutations' in PCR fragments of tumor DNA Gene 166 (2), 317-322 (1995) NCBI Similarity 23; Conser 96125211 Weghorst, C.M., Buzard, G.S., Calvert, R.J., Hulla, J.E. 366 52.6%; larity 88.5%; Conservative /note="this site within the pseudogene corresponds t translation stop site of the rat p53 cDNA; putative" a 388 c 336 g 357 t /note="this region of the pseudogene of the rat p53 cDNA; putative" 206472 10 of the rat p53 cDNA; putative 1107..1109 of the rat p53 cDNA; putative" 938..1031 of the rat p53 883..937 /note="this region of the pseudogene of the rat p53 cDNA; putative" /note="this region of the pseudogene of the rat p53 cDNA; putative" 499..746 of the rat p53 cDNA; putative" 316..498 note="tunc suppressor; this region of the pseudogene nofential open reading frame; putative; NCBI gi: <168..>542 /note="this region of the pseudogene
of the rat p53 cDNA; putative" /note="this site within the pseudogene ATG translation start site of the rat p of the rat p53 cDNA; putative" /note="this region of the pseudogene 1032..1447 /note="this region of the pseudogene 747..882 /note="this region of the pseudogene HERCSDGDDQTPPPYPTPSILSG" VCYVHVLPSPKLAI LPAGEDMPCAVMGQLHTSNWHLCACHGI YKKSQHMTEVMRRCSH 206473" /note="this region of the pseudogene corresponds to /note="this region of the pseudogene corresponds to /strain="Fischer 344" /gene="p53 PG-III" translation="KVQRKPSKCQLLPHRNLELRPLSLLKNLSQLWLSSGLPAVSDNQ/ /db\_xref="PID:g206473" /codon\_start=1 /gene="p53 PG-III" /tissue\_type="liver" /sex="male" /organism="Rattus norvegicus" Location/Qualifiers Score 20; DB 91; Pred. No. 3.66e-02; 0; cDNA; putative" Mismatches DB 91; Ų. Length 1447; Indels corresponds corresponds corresponds corresponds corresponds corresponds corresponds p53 cDNA; putative" 0; and Rice, J.M. Gaps ç ţ ç ç ç ç 6 ç exon exon exon exon exon exon exon 0;

Search completed: Tue Mar  $25\ 02:42:11\ 1997$  Job time :  $64\ \text{secs}$ .

100

Mar 25 02:42

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:43:09 1997; MasPar time 59.14 Seconds 283.363 Million cell updates/sec

Tabular output not generated.

Title: >US-08-644-289-2

Perfect Score: Description: (1-38) from US08644289.seq

N.A. Sequence: 1 AGTCAGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38 TCAGTCCGGAATCTCAATTTCCTACGGGTACGATGTCT

Scoring table: TABLE default

Gap 10

Nmatch STD: Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database: Database: 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST17 28:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST33
33:EST33 34:EST34 35:EST25 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST41 42:EST42 43:EST43 44:EST44
45:EST45 52:EST55 53:EST53 54:EST46 61:EST46 62:EST56
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81:EST81 82:EST88 89:EST89 90:EST99 91:EST91 92:EST92
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120:EST120 125:EST125

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7 136:STS8 137:STS9 138:STS10 139:ueEST 140:gnEST1 141:gnEST2 142:gnEST3 143:gnEST4 144:gnEST5 145:gnEST6 145:gnEST6 145:gnEST6 145:gnEST6 145:gnEST7 147:gnEST8 148:gnEST9 149:gnEST10 150:gnEST11 151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST15 155:gnEST15 156:gnST5 157:enEST1 158:enEST2 159:enEST3 160:enEST4 161:enEST5 162:enEST6 163:enEST7 164:enEST8 165:enEST9 166:enEST0 167:enEST1 168:enEST9 166:enEST9 1 173:enSTS1 174:enSTS2 169:enEST13 170:enEST14 171:enEST15 172:enEST16

Statistics: Mean 7.360; Variance 1.481; scale 4.970

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. derived by analysis of the total score distribution.

#### SUMMARIES

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# ALI GNMENTS

망 KEYWORDS ORIGIN REFERENCE BASE COUNT FEATURES SOURCE ACCESSION DEFINITION AUTHORS Query Match 47.4%; Best Local Similarity 79.3%; Matches JOURNAL ORGANISM source 323 aggccttggaactnaaggatgtccaggct 351 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., g1014189 H61357 yu41a06.r1 Homo sapiens cDNA clone 236338 5' similar to gb; X54156\_rnal CELLULAR TUMOR ANTIGEN P53 (HUMAN);. H61357 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Contact: Wilson RK Unpublished (1995) Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Homo sapiens RI sites of a modified pT7T3 vector (Pharmacia). Library vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Female. 1st High quality sequence stops: 284 WashU-Merck EST Project Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and constructed by Bento Soares and M.Fatima Bonaldo. double-stranded cDNA was size selected, ligated to Eco RI adapters IMAGE This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, LLNL Email: est@watson.wustl.edu The WashU-Merck EST Project Eutheria; Archonta; Primates; Catarrhini; Hominidae; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; (Pharmacia), digested with Not I and cloned into the Not I and Eco clone=236338 primer=M13RP1 library=Soares ovary tumor NbHOT (bases 1 to 368) 314 286 1810 314 286 1800 94 Consortium (info@image.llnl.gov) for further information. Conservative <1..>368 /organism="Homo sapiens" /clone="236338" Location/Qualifiers 99 с 368 bp Score 18; DB 25; Pred. No. 9.68e-05; <u>.</u> 109 Mismatches g 61 <u>\_</u> 6; Louis, Length 368; S others 중 63108 06-ocT-1995 <u>.</u> Ното. Gaps 0;

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mRNA BASE COUNT RESULT LOCUS င့ ORIGIN FEATURES COMMENT REFERENCE SOURCE KEYWORDS NID DEFINITION TOCUS. ACCESSION Best Matches Query Match AUTHORS ORGANISM JOURNAL source 292 tagaatgggcatcctttaa 310 34 Local Similarity TAGCATGGGCATCCTTTAA 16 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. repetitive element;. H97804  $_{
m yw02f03.s1}$  Homo sapiens cDNA clone 251069 3' similar to contains High quality sequence stops: 240 Source: IMAGE Consortium, LLNL Unpublished (1995) Homo sapiens g1118689 Tel: 314 286 1800 Fax: 314 286 1810 4444 Forest Park Parkway, Box 8501, St. Louis, Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK Wilson, R. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Male. 2NbHM vector=pT7T3D (Pharmacia) with a modified polylinker human clone=251069 primer=m13 -40 forward library=Soares melanocyte HSC05H051 Email: est@watson.wustl.edu The WashU-Merck EST Project Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Albino. double-stranded cDNA was size selected, ligated to Eco RI adapters 18; This clone is available royalty-free through LLNL; contact the (Pharmacia), digested with Not I and cloned into the Not I and Eco lst strand cDNA was primed with a Not I - oligo(dT) primer (bases 1 to 323) 139 Consortium (info@image.llnl.gov) for further information. Conservative ខា <1..>323 a 66 c /note="human" /clone="251069" organism="Homo sapiens" Location/Qualifiers 44.78; 94.78; 187 G Score 17; DB 36; Pred. No. 1.89e-03; 0; 55 Mismatches Φ 61 \_ 1; Indels Length 323; ~ others MO 63108 <u>,</u> Gaps ٥. 드

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partial cDNA sequence; transcribed sequence fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                         No significant homology found with :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Normalization_method: Bento Soares, P.N.A.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-OCT-1994) to the EMBL/GenBank/DDBJ databases
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/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                         /sex="Female"
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Best Local Similarity 73.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGCATGGGCATCCTTTAACTCTAAGGCCTGACT 1
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
                                                                                                                                                                    human clone=117266 library=Stratagene lung (#937210)
vector=pBluescript SK- host=50LR cells (kanamycin resistant)
primer=-21m13 Rsite1=EccRI Rsite2=Xhol Normal lung tissue from a 7
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAC-3'; 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beier, D. and Brady, K. Unpublished (1995)
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                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Pharmacology
University of Colorado Health Sciences Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       host=E. coli XL1-Blue primer=M13 Reverse Rsite1=EcoR I Rsite2=Xho I
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                                                                                   Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                        Eucaryotae; Metazoa; Chordata;
                                                                                                                                                    5'-CTCGAGTTTTTTTTTTTTTTTTT-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tjs@tally.hsc.colorado.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 3032708637
Fax: 3032707097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Box C236,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Sikela JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse library=Mouse brain, Stratagene vector=Lambda ZAP
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Pred. No. 3.30e-02;
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    ) was constructed by

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Query Match 42.1%; Best Local Similarity 76.7%; source EST. g1124671 N20004 SP:PR22 YEAST P24384 PRE-MRNA SPLICING FACTOR RNA HELICASE ;. yx31d08.s1 Homo sapiens cDNA clone 263343 3' similar to Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project Unpublished (1995) Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Hillier, L., Clark, N., Dubuque, T., Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Homo sapiens RI sites of a modified pT/T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal N20004 High quality sequence stops: 249 Tel: Contact: Wilson RK Unpublished Albino. human clone=263343 primer=ml3 -40 forward library=Soares melanocyte This Source: IMAGE Consortium, LLNL Email: est@watson.wustl.edu Fax: 314 286 1810 Washington University School of Medicine WashU-Merck EST Project The WashU-Merck EST Project Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Eutheria; Archonta; Primates; Catarrhini; Hominidae; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; double-stranded cDNA was size selected, ligated to Eco RI adapters host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Male. 2NbHM vector=pT7T3D foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. (Pharmacia), digested with Not I and cloned into the Not I and Eco st strand cDNA was primed with a Not I - oligo(dT) primer (bases 1 to 311) 8 clone is available royalty-free through LLNL; contact the Forest Park Parkway, Box 8501, St. Louis, MO 63108 314 286 1800 Consortium (info@image.llnl.gov) for further information. Conservative a /note="human" /organism="Homo sapiens" /clone="117266" Location/Qualifiers (1995)c . (Pharmacia) with a modified polylinker Score 16; DB 127; Pred. No. 3.30e-02; 0; Mismatches 8 g 96 t Elliston, K., Hawkins, M., Length 293; 1 others Indels 15-DEC-1995 0; Ното. Gaps 0,

KEYWORDS SOURCE

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REFERENCE

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ACCESSION DEFINITION LOCUS RESULT BASE COUNT ORIGIN

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                   Query Match 42.1%; Best Local Similarity 83.3%;
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Best Local Similarity 94.4%;
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                                                                                                                                                                                                                                                                                                           Genexpress_library_idt: C;
Genexpress_sequence_idt: y1c-3bh01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning method: total mRNA was oligo-(dT) primed and directionally cloned \bar{5}' -> 3' into the HindIII -> NotI sites of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.P. 8, 94801 Villejuif Cedex France. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genexpress@genethon.fr
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                            /tissue_type="total brain"
                                                                                                                                                                                    Psychiatry Dept. Columbia University USA"
                                                                                                                                                                                                       /isolate="muscular atrophy patient"
/clone_lib="normalized infant brain cDNA from B.Soares,
                                                                                                   /dev_stage="3 months old"
45 c 62 g 119
                                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 3.30e-02;
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
                                                                                                                                                                                                                             genbank release 81 swissprot release 28.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 364)
Auffray, C., Behar, G., Bois, F., Boucher, C., da Silva, C.,
                                                                                                                                                                                                                                                                                No significant homology found with :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5^{\prime} -> 3^{\prime} into the HindIII -> NotI sites of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone Library from B. Soares, Psychiatry Dept. Columbia University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.R. Acad. Sci., III, Sci. Vie 318, 263-272 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-OCT-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genexpress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSC17C011
                                                                                                                                                                                                                                                                                                                                                            Genexpress_library_idt: C;
                                                                                                                                                                                                                                                                                                                                                                                       Normalization_method: Bento Soares, P.N.A.S in press;
                                                                                                                                                                                                                                                                                                                                                                                                                  Stretch_removed: nothing
                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequence colinear to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer: M13 reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing_method: single read, full automatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sebastiani-Kabaktchis, C. and Tessier, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Genexpress cDNA program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genexpress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genethon, B.P. 60, 91002 Evry Cedex France and Genetique
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   partial cDNA sequence; transcribed sequence fragment.
                                                                                                                                                                                                                                                                                                                               Genexpress_sequence_idt: y1c-17c01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMAGE: Integated molecular analysis of the human genome and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 364)
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                        110
                   ø
                                           /tissue type="total brain"
/clone_lib="normalized infant brain cDNA"
/sex="Temale"
                                                                                                                         /isolate="muscular atrophy patient"
                                                                                                                                                    /dev_stage="3 months old"
                                                                                                                                                                             /organism="Homo sapiens"
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                     51 c
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Matches

20;

Conservative

0;

Mismatches

Indels

<u>,</u>

Gaps

0

3.30e-02;

DB 40;

Length 364;

Query Match 42.1%; Best Local Similarity 83.3%;

Score 16; Pred. No. ·.

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Best Local Similarity 83.3%;
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R57637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute, 100 College St., Toronto, Ontario, M5G1L5 Tel:
4169788758 Fax: 4169785650 Email: liewcc@utcc.utoronto.ca Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myosin alkali light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: GGTGGCGACGACTCCTGGAGCC. NCBI gi: 827695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Liew CC Molecular Cardiology University of Toronto Banting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 30:293-298(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library";
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                                                                                                                                                                                                                                                                                             18 cagaccgtagagtttaaggaggcc 41
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                         light chain.
R57637
                                                                                          R57637 367 bp mRNA
F4425 Homo sapiens cDNA clone F4425 5'
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BP; 98 A; 75 C; 117 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Wector: Lambda gt22; Site 1: Not1; Site 2: Sal1; mRNA was purified from human fetal hearts (10-12 weeks). cDNA was constructed using a NotI-Oligo dT adaptor-primer. SalI adaptors were ligated, followed by digestion with Not1, for directioncloning into predigested lambda gt22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="F4425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Fetal heart"
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Pred. No. 3.30e-02;
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                                                                                          end similar to Myosin alkali
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                                                                                                                                23-MAY-1995
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REFERENCE AUTHORS Ş ORIGIN REFERENCE SOURCE Tocus 맒 BASE COUNT COMMENT KEYWORDS ACCESSION DEFINITION RESULT FEATURES SOURCE KEYWORDS TITLE TITLE ORGANISM Matches Query Match 42.1%; Best Local Similarity 83.3%; ORGANISM AUTHORS JOURNAL source 18 4 12 CAGGCCTTAGAGTTAAAGGATGCC 27 cagaccgtagagtttaaggaggcc 41 g827695 F4425 Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H., Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C. Analysis of Expressed Sequence Tags (ESTs) from Fetal and Adult Heart cDNA Libraries Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H., Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C. Analysis of expressed sequence tags from a fetal human heart cDNA Myosin alkali light chain. R57637 Vertebrata; Homo sapiens EST. Unpublished (1995) Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Homo sapiens were ligated, followed by digestion with NotI, for direction cloning into predigested lambda gt22. Method is described in J. Mol. Cell. Cardiol. (1994) 26, 1329-1333). mRNA was purified from human fetal hearts (10-12 weeks). cDNA was constructed using a NotI-Oligo dT adaptor-primer. SalI adaptors human clone=F4425 library=Fetal heart vector=Lambda gt22 host=E. Contact: Liew CC Genomics 30 Eukaryotae; Banting Institute, 100 College St., University of Toronto Molecular Cardiology Contact: Liew CC Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; coli Y1090 primer=GGTGGCGACGACTCCTGGAGCC Rsite1=NotI Rsite2=SalI library human. Fax: 4169785650 Tel: 4169788758 20; (bases 1 to 367) (bases 1 to 367) 86 Fetal heart Homo sapiens cDNA clone F4425 5' Conservative liewcc@utcc.utoronto.ca. മ /note="human" /organism="Homo sapiens" Location/Qualifiers /clone="F4425" (2), 293-298 mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Primates; Catarrhini; Hominidae; Homo 75 c 367 g Score 16; DB 88; Pred. No. 3.30e-02; 117 g 0; Mismatches mRNA 77 Toronto, Ontario, M5G1L5 4 Length 367; Indels 02-MAY-1996 end similar to SalI adaptors 0; Gaps 0;

Molecular Cardiology

Fax: 4169785650

University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758 .

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity 83.3%;
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                                                                                                                                                                                                                                                           Nishiguchi, S., Joh, T., Horie, K., Zou, Z., Yasunaga, T. and Shimada, K. A survey of genes expressed in undifferentiated mouse embryonal carcinoma F9 cells: characterization of low-abundance mNNAs
                                    Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g618877
EST(expressed sequence tag).
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                                                     3-1, Yamadaoka
Suita, Osaka, 565
                                                                                                                                       Division of Molecular Biomedicine
                                                                                                                                                                                 Kazunori Shimada
                                                                                                                                                                                                  Submitted (25-OCT-1993) to DDBJ by:
                                                                                                                                                                                                                         95096008
                                                                                                                                                                                                                                          J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse embryonal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS84E02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: GGTGGCGACGACTCCTGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: liewcc@utcc.utoronto.ca
                 Phone: 06-879-8325
                                                                                             Osaka University
                                                                                                                    Research Institute for Microbial Diseases
                                                                                                                                                            Department of Medical Genetics
                                                                                                                                                                                                                                                                                                                                                                  Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
                                                                                                                                                                                                                                                                                                                                             Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                        (bases 1 to 367)
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06-879-8326
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a 75 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: Lambda gt22; Site 1: Not1; Site 2: Sal1; mRNA was purified from human fetal hearts (10-12 weeks). cDNA was constructed using a Not1-Oligo dT adaptor-primer. Sal1 adaptors were ligated, followed by digestion with Not1, for direction cloning into predigested lambda gt22. Method is described in J. Mol. Cell. Cardiol. (1994) 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. coli Y1090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Fetal heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="F4425"
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                                                                                                                                                                                                                                        116 (1),
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Pred. No. 3.30e-02;
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84E02.
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Mar 25 02:42 US-08-644-289-2.rst

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ç B Ş В RESULT ORIGIN BASE COUNT FEATURES Matches Matches Query Match 42.1%; Best Local Similarity 83.3%; Best Local HS290ZB5 Z51281; /note="cloning vector is M13mp18" Sequence 373 BP; 132 A; 87 C; 53 G; 95 T; 6 other; DID C., Faure S., Fizames C., Samson D., Drouot N., Vignal A., Millasseau P., Marc S., Hazan J., Seboun E., Lathrop M., Gyapay G., Morissette J., Weissenbach J.; H.sapiens (D2S2334) DNA segment containing (CA) repeat; clone source source Nature 380:152-154(1996). microsatellites" Jean.Weissenbach@genethon.fr Genethon, B.P. 60, 91002 Evry Cedex France. E-mail: Submitted (01-SEP-1995) to the EMBL/GenBank/DDBJ databases. Weissenbach J.; 1 - 373Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Homo sapiens (human) microsatellite marker; repeat polymorphism; STS. CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; AFM290zb5; single read. 22-MAR-1996 (Rel. 47, full automatic; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. 18-MAR-1996 (Rel. 47, Created) A comprehensive genetic map of the human genome based on 5,264 80 catgggccacctttaaaattaaagcctg 107 31 5 00 CATGGGCATCCTTTAACTCTAAGGCCTG h 42.1%; Similarity 78.6%; 20; 22; 124 a standard; DNA; STS; 373 Conservative Conservative /organism="Homo sapiens" /cell\_line="CEPH 134702" /clone\_lib="genomic DNA" 1..373 /organism="Mus musculus"
/cell\_line="mouse embryonal carcinoma cell line
/cequenced\_mol="cDNA to mRNA"
/sequenced\_mol="cDNA to mRNA"
12 c 114 g 56 t 1 others Location/Qualifiers /chromosome="2" Location/Qualifiers Last updated, Version 3) = = = Score 16; DB 52; Pred. No. 3.30e-02; Pred. No. 3.30e-02; Score 16; 114 g **0**; 0; 31 Mismatches Mismatches ВP DB 173; Length 373; 4; 6, Length 367, Indels Mammalia; <u>,</u> 0; Gaps Gaps F9" 0; 0

JOURNAL COMMENT REFERENCE AUTHORS REFERENCE AUTHORS TITLE RESULT LOCUS မ SOURCE ACCESSION 뭉 BASE COUNT FEATURES KEYWORDS DEFINITION Query Match
42.1%; Score 16; DB 135; Length 373;
Best Local Similarity 78.6%; Pred. No. 3.30e-02;
Matches 22; Conservative 0; Mismatches 6; Indels TITLE ORGANISM JOURNAL 15 HSZYUZBS 373 bp DNA STS 22-MAR-1996 H.sapiens (D2S2334) DNA segment containing (CA) repeat; clone AFM290zb5; single read. Nature 380, 152-154 (1996) Homo sapiens full automatic. A comprehensive genetic map of the human genome based on 5,264 microsatellites Dib,C., Faure,S., Fizames,C., Samson,D., Drouot,N., Vignal,A., Millasseau,P., Marc,S., Hazan,J., Seboun,E., Lathrop,M., Gyapay,G., Morissette,J. and Weissenbach,J. Direct Submission
Submitted (01-SEP-1995) Genethon, B.P. 60, 91002 Evry Cedex France.
E-mail: Jean.Weisenbach@genethon.fr CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism; STS. Weissenbach, J. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 373) g1232581 human. (bases 1 to 373) 132 a /organism="Homo sapiens"
/note="cloning vector is M13mp18"
/cell\_line="CEPH 134702"
/clone\_lib="genomic DNA"
/chromosome="2"
2 a 87 c 53 g 95 t 6 c 1..373 Location/Qualifiers 53 g 6 others Indels 0; Gaps <u>,</u>.

Search completed: Tue Mar 25 02:44:17 1997 Job time : 68 secs.

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\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* (HE)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_nn n.a. ı n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:47:33 1997; MasPar time 8.73 Seconds 279.817 Million cell updates/sec

Tabular output not generated.

Description: Title: (1-28) from US08644289.seq >US-08-644-289-3

N.A. Perfect Score: Sequence: 1 AGTCGAATTCATTGGGACCATCCTGGCT 28

TCAGCTTAAGTAACCCTGGTAGGACCGA

Scoring table: TABLE default

Gap

Nmatch STD : Dbase 0; Query 0

113505 seqs, 43611913 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

n-geneseq25

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.755; Variance 3.299; scale 1.744

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score		Query Match Length DB	DB	ID	Description	Pred. No.
1	28		100.0 28 21 T10	21	T10487	Human wild-type p53 g	7.90e-07
c 2	23	82.1	91	9	Q51746	Oligonucleotide probe	8.59e-04
ω	20	71.4	91	9	Q51746	Oligonucleotide probe	4.74e-02
c 4	16	57.1	184	σ	Q39756	Expressed Sequence Ta	7.34e+00
ი 5	16	57.1	184	∞	Q59168	Human brain Expressed	7.34e+00
c 6	16	57.1	280	ထ	Q61255	Human brain Expressed	7.34e+00
7	16	57.1	303	6	Q39930	Expressed Sequence Ta	7.34e+00
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13 9 7	12 5 4 21	2 4 2 2 1	2288	15 18 20 19 10 6	- 6 2 6 6	17	льюют	o
Q75209 Q51024 Q44278	Q14263 Q71479 Q78568 Q28591 T18877	Q03369 N92451 N70974 Q24257 N71063	Q59313 Q59197 Q05617 Q11820	Q92775 T13451 T26961 T16883 Q58708 Q36952 N81164	Q55095 N50521 N71120 N50531 Q06900	N92579 N36395 T11549	Q39880 Q39892 Q59292 Q53209	
<b>-</b> <	p-meta-l metastasis-s Consensus sequence of Human thrombin recept Lipoxygenase structur Human TCL-l gene.	Sequence encoding hum cDNA insert of vector Sequence of human atr Branching enzyme DNA. Genomic sequence enco	brain Expres brain Expres for porcine ninogen activa		Degenerate oligo for Sequence encoding sal Sequence encoding pig Plasmid pPE603. Neo-pullulanase gene.	Sequence of the 1.7kb Benzene dioxygenase g Tumour rejection anti	rai ycl	Himan brain Evarence
7.64e+01 7.64e+01 7.64e+01	7.64e+01 7.64e+01 7.64e+01 7.64e+01 7.64e+01 7.64e+01	7.64e+01 7.64e+01 7.64e+01 7.64e+01 7.64e+01				7.34e+00 7.34e+00 7.34e+00 7.34e+00		7 3/0+00

## ALI GNMENTS

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individual treatment regimes.

Disclosure; Page 7; 40pp; English.

T10486-T10488 are primers used in a RT-PCR reaction to obtain an N-terminal (nuclcotides -111 to 1090) portion of the wild-type p53 gene. An epitope from intron 10 of the human p53 gene is used to
                                                                                                                                                                                                                                                                                  Tumour suppressor; p53; alternative splicing; antibody; cancer; proliferative disorder; psoriasis; prognosis; diagnosis; cell cycle;
                                                                                                                                                                                                                                                                                                                                  03-0CT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                         T10487;
                                                                                           useful
                                                                                                          New antibodies specific for alternatively spliced mammalian p53
                                                                                                                            WPI; 96-140137/15.
                                                                                                                                              Kulesz-Martin MF;
                                                                                                                                                            (HEAL-) HEALTH RES INC.
                                                                                                                                                                                14-JUN-1994; US-259612
                                                                                                                                                                                                05-JUN-1995;
                                                                                                                                                                                                                                    CA2150994-A.
                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                    reverse transcriptase polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                     Human wild-type p53 gene N-terminal RT-PCR sense primer.
                                                                                                                                                                                                                                                                                                                                                                       T10487 standard; DNA;
                                                                                                                                                                                                                  5-DEC-1995.
                                                                                         in diagnosis or prognosis of cancer, and for establishing
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US-08-644-289-3 mg

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DT 31
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ULT 2
Q51746 standard; cDNA; 91 BE
Q51746;
31-MAY-1994 (first entry)
                       Synthetic.
EP-571911-A.
01-DEC-1993.
                                                                                                              88.
                                                                                                                                                                                                                     LT 3
Q51746 standard; cDNA;
Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cross reacted to a few non-mycobacterial spp. The probe mabe useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be used in gene therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (p53as) and their expression. When the antibodies are injected into cells they may cause cell cycle arrest. Vectors contg. p53as cDNA may
24-MAY-1993; 108325
                                                                                                                                     Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                             Oligonucleotide probe MK14-A
                                                                                                                                                                                           31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shank DD, Spears
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAY-1993; 108325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP-571911-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of human cancer and in the study of p53 and alternatively spliced p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spliced p53. The antibodies are useful in the diagnosis and prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     create antibodies directed against this sequence in an alternatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection and amplification of Mycobacteria nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligo:nucleotide probes specific for Mycobacteria - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.1%;
0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 A;
                                                                                                                                                                                                                                               91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 9; L
Pred. No. 8.59e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 7.90e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                               Query Match 57.1%;
Best Local Similarity 94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 0; Conser
                                                 Matches
                                                                                                              from the ESTs) sublocalisation of an EST can be achieved with fragments from specific chromosomes or pools of large genomic an analogous manner. This sequence represents EST00322. Sequence 184 BP; 40 A; 52 C; 45 G; 47 T;
                                                                                                                                                                                                                                                                                                                                                               19-JUN-1992; U05222.
20-JUN-1991; US-716831.
12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH 6 HUMAN SERVICE.
Adams MD, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q39756 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide probe MK14-A consists of nucleotides 5-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shank DD, Spears WFI; 93-378844/48.
                                                                                                             Sequence
                                                                                                                                                                            genes within a few years at a fraction of the cost of complete genomic sequencing. Using PCR primers 039419-039580 (sequences designed
                                                                                                                                                                                                                                                                                                                 Particular expressed sequence tags from human CDNA - corresponds to transcription prods. of genes, useful for tagging genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human gene sequencing; PCR mapping; somatic cell hybrids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed sequence tag; human genome project; chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cross reacted to a few non-mycobacterial spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                               DNA sequence tagged sites (STSs), ESTs point directly to expressed genes. The use of ESTs could facilitate the tagging of most expressed human
                                                                                                                                                                                                                                                               This sequence represents an EST (expressed sequence tag) ESTs are markers
                                                                                                                                                                                                                                                                                Claim 3; Page 127; 199pp; English.
                                                                                                                                                                                                                                                                                                 mapping chromosomes and tissue typing
                                                                                                                                                                                                                                                                                                                                                   WPI; 93-036325/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ю9300353-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sublocalisation; gene tagging; tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed Sequence Tag human gene marker EST00322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be useful as an initial screen for mycobacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (051735). It hybridized to all spp. of mycobacteria tested,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                 for human genes actually transcribed in vivo. Unlike the random genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BECT ) BECTON DICKINSON
                 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 hsvhhvvhhvhvsvvvvhhvvhvvhh 51
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agccaggatggtctcaat 180
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.larity 0.0%;
Conservative
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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                                                              Score 16; DB 6; L
Pred. No. 7.34e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20; DB 9; Len Pred. No. 4.74e-02; 23; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 C;
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                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 G;
                                                1:
                                                                             Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 T;
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                                                 Indels
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clones in
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The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 6
Q61255 standard; DNA; 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST00322 has a "poor" coding probability as evaluated using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                        of most human genes
                                                                                                                                                                                                                                                     Adams MD, Moreno RF, WPI; 93-272882/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                        W09316178-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coding-region prediction program CRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on chromosomes, for individual or forensic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 132; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of most human genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           markers for human genes transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams MD, Moreno RF, Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICE Adams MD, Moreno RF, Venter CJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9316178-A.
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                                                                                                                            Example 4; Page 462; 500pp; English.
                                                                                                                                                                                        markers for human genes transcribed in-vivo, facilitate tagging
                                                                                                                                                                                                                  Enriched oligonucleotides and corresp. sequences - used as
                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                        12-FEB-1993; U01294.
12-FEB-1992; US-837195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription; mapping; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene transcription product; genetic markers; tagging; in vivo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain Expressed Sequence Tag EST01742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also Q59041-Q61440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tagging of most human genes, for mapping locations of expressed genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for human genes transcribed in vivo. They can be used to facilitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enriched oligonucleotides and corresp. sequences - used as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription; mapping; locations; chromosomes; chromosomal; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene transcription product; genetic markers; tagging; in vivo;
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                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-1993; U01294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 agccaggatggtctcaat 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%;
94.4%;
                                                                                                                                                                                                                                                                                    Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16; DB 8; I Pred. No. 7.34e+00;
                                                                                                                                                                                                                                                                                    ខ្ម
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in-vivo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 G;
  locations of expressed genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        facilitate tagging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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888888 Ş 밁 ç В Mar 25 02:45 Query Match 57.1%; Best Local Similarity 94.4%; Query Match 57.1%; Best Local Similarity 94.4%; Matches Matches for human genes actually transcribed in vivo. Unlike the random genomic DNA sequence tagged sites (STSs), ESTs point directly to expressed genes. The use of ESTs could facilitate the tagging of most expressed human genes within a few years at a fraction of the cost of complete genomic sequencing. Using PCR primers 039419-039580 (sequences designed from the ESTs) sublocalisation of an EST can be achieved with panels of fragments from specific chromosomes or pools of large genomic clones in Human brain Expressed Sequence Tag EST00312. Gene transcription product; genetic markers; tagging; mapping chromosomes and tissue typing Claim 3; Page 189; 199pp; English. Q39930 standard; coding-region prediction program CRM. Sequence 280 BP; 61 A; 62 C; type, and for prepn. of antisense sequences, probes and constructs. EST01742 has a "poor" coding probability as evaluated using the Q59342; Q59342 standard; Sequence 07-JAN-1993. 19-JUN-1992; U05222. 20-JUN-1991; US-716831. expressed sequence tag; human genome project; chromosome; Expressed Sequence Tag human gene marker EST00312. on chromosomes, an analogous manner. This sequence represents EST00312. This sequence represents an EST (expressed sequence tag) to transcription prods. of genes, useful for tagging genes, Particular expressed sequence tags from human CDNA - corresponds WPI; 93-036325/04. Adams MD, Synthetic. sublocalisation; gene tagging; tissue typing. human gene sequencing; PCR mapping; somatic cell hybrids; 20-MAY-1993 (first entry) locations of disease-associated genes, for identification of tissue (USSH ) US DEPT HEALTH & HUMAN SERVICE. ¥09300353-A. 6-MAR-1994 (first entry) 259 attgagaccatcctggct 276 2-FEB-1992; US-837195 1 28 44 agccaggatggtctcaat 61 ATTGGGACCATCCTGGCT AGCCAGGATGGTCCCAAT 11 17; Venter JC; 303 BP; Conservative Conservative for individual or forensic identification, for mapping DNA; cDNA; 303 102 A; 28 BP ₽P. Pred. No. 7.34e+00; Pred. No. Score 16; Score 16; US-08-644-289-3 mg <u>.</u>. 53 C; Mismatches 7.34e+00; See also Q59041-Q61440. 49 G; 107 T; DB 6; DB 8; 67 G; Length 303; ۲. Length 280; 1; Indels 79 T; in vivo; ESTs are markers 0; <u>,,</u> Gaps Gaps <u>,</u> 0;

transcription; mapping; locations;

chromosomes;

US-08-644-289-3.mg

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16-MAR-1994
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type, and for prepn. of antisense sequences, probes and constructs. EST01770 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also Q59041-Q61440. Sequence 342 BP; 60 A; 100 C; 88 G; 93 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue
                                                                                                                                                                                                                                                                           The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers
                                                                                                                                                                                                                                                                                                                                               Example 4; Page 472; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         of most human genes
                                                                                                                                                                                                                                                                                                                                                                                                                      Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging
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                                                                                                                                                                              on chromosomes, for individual or forensic identification, for mapping
                                                                                                                                                                                                           for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 93-272882/34.
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WO9316178-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding-region prediction program CRM.
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12-FEB-1993; U01294.
12-FEB-1992; US-837195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams MD, Moreno RF, Venter CJ.
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12-FEB-1992; US-837195.
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                                                                                                                                             locations of disease-associated genes, for identification of tissue
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Local Similarity 94.4%;
hes 17; Conservative
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Pred. No. 7.34e+00;
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Query Match

57.1%;

Score 16;

DB 8;

Length 342;

RESULT ID Q AC Q AC Q DT 1 DE H DE H CKW G KW G KW G FPD 1 PPD 1 P	Qu Be Ma Db	RESULT ID SULT TO SULT	Best Match Db 1
IT 11 Q59292 standard; cDNA; 406 BP. Q59292; 16-MAR-1994 (first entry) Human brain Expressed Sequence Tag EST00337. Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss. Homo sapiens. W09316178-A. 19-AUG-1993. 112-FEB-1993; U01294. 112-FEB-1993; US-837195. (USSH ) US DEPT HEALTH & HUMAN SERVICE. Adams MD, Moreno RF, Venter CJ. WPI; 93-272882/34.	Query Match 57.1%; Score 16; DB 6; Length 406; Best Local Similarity 94.4%; Pred. No. 7.34e+00; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 171 attgagaccatcctggct 188	Q39880; standard; DNA; 406 BP. Q39880; 20-MAY-1993 (first entry) Expressed Sequence Tag human gene marker EST00337. expressed Sequence tag; human geneme project; chromosome; human gene sequencing; PCR mapping; somatic cell hybrids; sublocalisation; gene tagging; tissue typing. Synthetic. W0390353-A. W0390353-A. W0390353-A. W0390353-A. W1-JNN-1991; US-716831. 12-FEB-1992; US-837195. WSSH) US DEPT HEALTH & HUMAN SERVICE. Adams MD, Venter UC; WPI; 93-036325/04. Particular expressed sequence tags from human CDNA - corresponds to transcription prods. of genes, useful for tagging genes, mapping chromosomes and tissue typing Claim 3; Page 171; 199pp; English. This sequence represents an EST (expressed sequence tag) ESTs are markers for human genes actually transcribed in vivo. Unlike the random genomic DNA sequence tagged sites (STSs), ESTs point directly to expressed man genes within a few years at a fraction of the cost of complete genomic sequencing. Using PCR primers Q39419-Q39580 (sequences designed from the ESTs could facilitate the tagging of most expressed man genes within a few years at a fraction of the cost of complete genomic sequencing. Using PCR primers Q39419-Q39580 (sequences designed from the ESTs) sublocalisation of an EST can be achieved with panels of fragments from specific chromosomes or pools of large genomic clones in an analogous manner. This sequence represents EST00337. Sequence 406 BP; 103 A; 109 C; 114 G; 77 T;	Best Local Similarity 94.4%; Pred. No. 7.34e+00; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 163 agccaggatggtctcaat 180

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RESULT 13
ID Q31877 standard; DNA; 2022 BP
AC Q31877;
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Best Local Similarity 94.4%;
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Best Local Similarity 94.4%;
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The sequence is that of a human cyclin D3 pseudogene.
Sequence 2020 BP; 553 A; 485 C; 463 G; 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New D-type mammalian cyclin - replaces CIN-type protein needed for cell start in budding yeast and is detected by antibodies or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-type; mammalian; CLN protein; protein deficiency; cell cycle start;
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26-MAY-1992; US-888178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybridisation in biological samples to determine abnormal cell
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                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                            1; Indels
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/note= "A to (
W09220796-A.
                                                                                                                                                    cycle or that they do not undergo destruction. The human cyclin D genes share very high similarity over their entire coding region: 6 between D1 and D2, 60% between D2 and D3 and 52% between D1 and D3.
                                                                                                                                                                                                                                                                                                                                                                                   Recombinant mammalian D-type cyclin - replaces a CLN-type protein essential for cell start in budding yeast, its antibodies and probes being useful in detecting D-type cyclin in biological
                                                                                                                                                                                                                                                                                                     Disclosure; Fig 10; 75pp; English.
The sequences given in Q31876-77 represents the cyclin D2 and D3 pseudogenes. These sequences were identified during the chromosomal localisation of the D2 and D3 genes. These genes were contained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "Frameshift mutation"
1679
                                                                                          Sequence
                                                                                                       See also Q31873-75.
                                                                                                                       but are less closely related than the cyclin A and cyclin E genes.
                                                                                                                                     The cyclin D genes are more closely related than the cyclin B genes
                                                                                                                                                                                                different mechanism to govern their periodic degradation during cell
                                                                                                                                                                                                             and B-type cyclins which targets them for ubiquitin-dependant degradation. This suggests that the D-type cyclins have evolved a
                                                                                                                                                                                                                                                             a similar small size protein ranging from 289-295 amino acids.
                                                                                                                                                                                                                                                                          novel D-type cyclins disclosed by this invention were shown to encode
                                                                                                                                                                                                                                                                                         within clones lambdaD2-G1 and lambdaD3-G5 respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 92-415774/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beach DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_type= Direct_duplication
mutation 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutation
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repeat_unit 1379..1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= d
/note= "Frameshift mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Nonsense mutation" mutation 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ubiquitin-dependant; degradation; similarity; D1; E; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclin; D2; D3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclin D3 pseudogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1993
                                                                                                                                                                                                                                                lack the "destruction box" identified in the N-terminus of both A-
                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; R29314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COLD-) COLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8-MAY-1992; U04146
827 agccaggatggtctcaat 844
                                           Similarity
                                                                                            2022 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPRING HARBOR LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G mutation*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lambdaD2-G1; lambdaD3-G5; destruction box; A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                         57.18;
94.48;
                                                                                         554 A;
                           Pred. No. 7.34e+00;
0; Mismatches 1
                                                          Score 16;
                                                                                          487
                                                                                          ς:
                                                          DB 5;
                                                                                          463 G;
                                                          Length 2022;
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AGCCAGGATGGTCCCAAT 11

IT 14 N92579 standard; DNA; 3094 BP.

N92579;

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EP-34808-A.
06-DEC-1989.
02-UN-1989; 110056.
03-UN-1988; US-202721.
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Sequence of the 1.7kb cDNA molecule encoding antibodies 7D1,7D4 and 20C6.
                              /note=
CDS
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Q36395 standard; DNA; 4721 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Fig 20A-D; 78pp; English.
The inventors claim a new protein which comprises one or more immunoreactive and/or antigenic determinants of an Eimeria surface antigen of mol. wt. 28,37,120 or more than 200 kD which specifically
                                                                                                             Sgo
                                                                                                                                      /note=
                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                  Benzene dioxygenase gene region.
Benzene; dioxygenase; cysbenzene glycol; transformation; BDO;
                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be enhanced by inserting additional genes into the carrier virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see P93703-6). Also new are DNA encoding the protein (see N92576-9), and a vaccine comprising one or more proteins. Vaccine utility can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Altenburger W, Binger MH, Chizzonite RA, Kramer RA, Lomedico PT, McAndrew SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eimeria.
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                                                                              /*tag=
                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q36395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binds to one or more monoclonal antibody (MaB) from ATCC HB 9707-9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coccidiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pox:virus vectors as a vaccine to protect chicks against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequences encoding Eimeria surface antigens - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; P93706.
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     *tag=
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                           "Benzene dioxygenase gene III"
3084..3413
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                                                                                                                                                                                                                                                                                                                                aeruginosa.
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llarity 80.8%;
Conservative
                                                                                                          dioxygenase
2591..2998
                                                                                                                                                                                            dioxygenase gene
1912..2553
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Pred. No.
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; 7.34e+00;
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                                                        Query Match 57.1%;
Best Local Similarity 94.4%;
                                               Matches
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-10_signal
/*tar-
                                                                                         glycol dehydrogenase gene and catechol 2,3-oxygenase gene Claim 11; Page 12-18; 20pp; Japanese.

This sequence encodes five regions of a benzene dioxygenase (BDO) polypeptide. Cysbenzene glycol can be produced effectively from benzene using transformants prepared using this fragment.

Sequence 4721 BP; 917 A; 1382 C; 1494 G; 928 T;
            1524 tggtcccaatgaaatcga 1541
                                                                                                                                                         WPI; 93-054795/07.
P-PSDB; R32085-89.
Microbe DNA - contg. benzene di:oxygenase gene, cis:benzene
                                                                                                                                                                                                                                                   /*tag= g
J05003785-A.
                                                                                                                                                                                                                            30-OCT-1991;
                                                                                                                                                                                                                                       14-JAN-1993.
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                                                                                                                                                                                                                 6-APR-1991;
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 TGGTCCCAATGAATTCGA 3
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                                              17;
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JP-084170.
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479..484
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                                                        Score 16; DB 6; L
Pred. No. 7.34e+00;
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Search completed: Tue Mar 25 02:47:48 1997 Job time : 15 secs.

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\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \* (ME)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:46:12 1997; MasPar time 54.01 Seconds 426.945 Million cell updates/sec

Tabular output not generated.

Title: >US-08-644-289-3

Perfect Score: N.A. Sequence: Description: Comp: (1-28) from US08644289.seq 1 AGTOGAATTCATTGGGACCATCCTGGCT 28 TCAGCTTAAGTAACCCTGGTAGGACCGA

Scoring table: TABLE default

Gap

Nmatch STD: Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database: Database: genbank 94 1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PIN 9:PRI 10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7 23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:IVV4 29:INV5 30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2 37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLM1 43:PLM2 44:PLM3 45:PLM4 46:PLM5 47:PLM6 48:PLM7 49:PLM8 50:PR11 51:PR12 52:PR13 53:PR14 56:PR15 55:PR16 56:PR17 57:PR18 58:PR15 59:PR110 60:PR111 61:PR112 62:PR113 63:ROD1 64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8 71:STR 72:SYM 73:IMA 74:VRL1 75:VRL2 76:VRL3 77:VRL4 78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database:

genbank-new5 82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG 89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

Database:

u-emb146\_94

Statistics: Mean 7.337; Variance 2.794; scale 2.626

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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H.sapiens G6PD gene f Human DNA sequence fr Human DNA sequence fr Homo sapiens chromoso	ence f	Human DNA sequence fr	rhabditis	rhabditis		Human cosmid N79E2.	Human Cosmid N73F4	0 0	ANG	DNA sequence	ence	Human gene for ATP sy	Human 4-hydroxyphenyl		omonas sp. bip	Human DNA seguence fr	Down Syndrome	DNA s	Down Syndrome	Na+, K+ A	thyroid	Q.	(clon	DNA	H saniens DNA loom at	Homo saniens (clones:	Brachydanio rerio (vh	A.anguilla mRNA for s	R.americanum chloropl		mRNA	p53 cellu		genomi	Murine gene fragment	tumor antigan	Description	
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### ALIGNMENTS

ORGANISM	KEYWORDS SOURCE	NID	ACCESSION	DEFINITION	LOCUS	RESULT 1
Mus musculus Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;	Mouse DNA.	g191973	M26862	Mouse tumor antigen p53 gene, 5' end.	MUSANTP53 536 bp DNA	
Chordata;			•	p53 gene,	DNA	
Vertebrata,				5' end.	ROD	
, Mammalia;						
Theria;					15-DEC-1989	

REFERENCE

AUTHORS TITLE

Bienz-Tadmor, B., 2akut-Houri, R., Libresco, S., Givol, D. and O: The 5' region of the p53 gene: Evolutionary conservation and evidence for a negative regulatory element

Givol, D. and Oren, M.

Eutheria; Rodentia; Myomorpha; Muridae; Murinae. 1 (bases 1 to 536)

JOURNAL

EMBO J.

4, 3209-3213 (1985)

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JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
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DEFINITION
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ORIGIN
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Best Local Similarity 100.0%;
Matches 21; Conservative
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Best Local Similarity 100.0%;
Matches 21; Conservative
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Bienz, B., Zakut-Houri, R., Givol, D. and Oren, M.
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Locus FEATURES REFERENCE SOURCE ACCESSION DEFINITION RESULT ORIGIN BASE COUNT FEATURES REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION KEYWORDS LOCUS Query Match 75.0%; Best Local Similarity 100.0%; Matches 21; Conservative JOURNAL MEDLINE TITLE ORGANISM TITLE ORGANISM JOURNAL AUTHORS AUTHORS MEDLINE source misc\_feature intron source g53572 Mouse Mouse p53 mRNA, complete cds, clone pcD53. Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol,D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306 (5943), 594-597 (1983) Mus musculus X01235 Eukaryota; Animalia; Chordata; Eutheria; Rodentia; Myomorpha; 1 (bases 1 to 1285) Mus musculus p53 gene antigen. Rotter, V. Arai, N., Nomura, D., Yokota, K., Wolf, D., Brill, E., Shohat, O. and pCD-p53. Mouse (BALB/c) nontransformed helper T-cell, cDNA to mRNA, clone g200198 MUSP53A 84068204 Sciurognathi; Myomorpha; Muridae; Murinae; Mus. Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; MMP53G1 87064640 Mol. Cell. Biol. 6, splicing Immunologically distinct p53 molecules Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; house mouse. (bases 1 to 554) 130 a genomic /note="pot. 531..554 /organism="Mus musculus"
1..530 /sub\_species="domesticus" /strain="BALB/c" /organism="Mus musculus" /note="pot. 1..554Location/Qualifiers Location/Qualifiers 154 c 1285 bp DNA 554 for 5' 3232-3239 (1986) exon" Score 21; DB 64; Pred. No. 4.30e-03; intron" 0; 126 g mRNA DNA region of cellular Mismatches 144 t Vertebrata; Mammalia; Muridae; Murinae. <u>,</u> generated by alternative Length 554; tumour antigen p53. 07-NOV-1985 0 Choanata, Gaps Chordata; 0

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                                                                                                                                                                                                                                                      sequence of cDNA in [1] was established by analysing four separate cDNA clones; p176 (bp 1-1247), p271 (bp 69-638), p422 (bp 1288-1719), and p208 (bp 1432-1719) [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                           proteins are rich in proline, contain proline runs or clusters, and are localized in the nucleus of tranformed cells. The Ela proteins and p53 have been shown to have very short half-lives [2]. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pennica, D., Goeddel, D.V., Hayflick, J.S., Reich, N.C., Anderson, C.W.
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  substitutions and to some
                             the two sequences differ by only 4%. The differences are due to
                                                     nucleotide 186 onward. Upstream of this position the two sequences deverge totally and no homology can be observed; downstream of here
                                                                                                                                        sequence of the murine p53 psuedogene, also reported by [1] (see
                                                                                                                                                                     gene, mostly due to post-translational modifications [1].
                                                                                                                                                                                                   existing different forms of murine p53 must be products of the same
                                                                                                                                                                                                                                There is only one functional p53 gene in the mouse genome. All
                                                                                                                                                                                                                                                                                                                                                                                                                              products and the adenovirus Ela proteins. All three of these
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                                                                                                             separate entry), and the cDNA sequence are almost identical from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1716)
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Submitted (28-NOV-1985) to the EMBL/GenBank/DDBJ databases
                  Direct Submission
                                       Givol, R.
                                                                                               EMBO J. 3 (9), 2179-2183 (1984)
                                                                                                                                       Analysis of the gene coding for the murine cellular tumour antigen
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<1..1668</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="PID:g200205"
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/product="cellular tumor antigen"
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Pred. No. 4.30e-03;
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#### FEATURES COMMENT REFERENCE ORGANISM JOURNAL AUTHORS source repeat\_region repeat\_region repeat\_region repeat\_region misc\_feature repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region true left end of clone L185F6 is at 31621 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, constructed using flow-sorted human chromosome 4 from a Hamster-Human hybrid cell line ( $\tt UV20HL21-27$ ) containing human chromosomes 4, 8 and 21. Williamson, H. Homo sapiens L196E3 is contained in a clone contig spanning 2Mb which is described in Baxendale et al, Nature Cenetics 4 (1993) auspices of the U.S. Department of Energy. The library was such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the The true left end of clone L196E3 is at 1 in this sequence. humpub@sanger.ac.uk CB10 1RQ, England. E-mail enquires regarding this sequence: Submitted (31-OCT-1995) Sanger Centre, Hinxton, Cambridgeshire, Eukaryotae; VECTOR: sCosl Genome Center, sequence is ambiguous, there is an annotation using the 'unsure' submissions. shorter because we only sequence overlapping sections once, This sequence is not the entire insert of clone L196E3. IMPORTANT: Direct Submission Vertebrata; 196E3 is from cosmid library LAO4NCO1 constructed at the Human eature key. longer because we arrange for a small overlap between neighbouring 218-230 181- 186. (bases 1 to 31720) /note="Alu 1987..2278 /note="Alu 2575..4365 /note="Alu repeat: matches 1..308 of consensus" 4252..4413 /note="Alu repeat: matches 1553..1846 958..1248 323..612 /cell 3235..3459 /map="4p16.3" 3462..3749 /note="MER42C element fragment" 3093..3146 1262..1546 /note="Alu repeat: matches 1..308 of consensus" /note="L1 element fragment" 229..319 /clone\_lib="LA04NC01" /clone="L196E3" /chromosome="4" /organism="Homo sapiens" Location/Qualifiers 'note="MER42C element fragment" note="match: cDNA D25266" 'note="Alu repeat: matches 308..1 of consensus" mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Primates; Catarrhini; Hominidae; Homo See also Myers et al, Cytogenet Cell Genet. 66 ( 1994 Los Alamos National Laboratory, NM 87545 under the line="UV20HL21-27" repeat: matches 308..1 of consensus" repeat: matches 1..308 of consensus 308..1 of consensus" It may be

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/note="MER42C element fragment"
4561..4854

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21939..22228
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9498..9591
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5744..5794
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complement(14579..16027)
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8172..8342
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6411..6582
   /note="Alu repeat: matches 1..308 of consensus" 24223..24306
                                       /note="Alu repeat: matches 11..308 of
23768..24071
                                                                          /note="Alu repeat: matches 42..143 of 23258..23538
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23109..23205
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23074..23108
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14100..14303
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12498..12613
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12416..12478
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10969..11257
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13742..13846
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13089..13418
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/note="Alu repeat: matches 144..1 of consensus"
a 7283 c 7157 g 7628 t
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/note="L1 element f
30243..30521
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30679..30805
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28459..28557
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27610..27730
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27408..27523
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27248..27407
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24378..24527
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28142..28398
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28089..28134
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26141..26314
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25853..26140
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25205..25361
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24895..25202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Savolainen, V., Manen, J.F., Douzery, E. and Spichiger, R. Molecular phylogeny of families related to Celastrales based
                                                      1 (bases 1 to 1147)
Cutler,C., Sanders,I.L. and Cramb,G.
                                                                                                                                                                                                                                                         g496529
                                                                                                                                                                                                                                                                               X76109
                                                                                                                                                                                                                                                                                              A.anguilla mRNA for sodium/potassium ATPase, beta subunit.
                                                                                                                                                                                                                                                                                                                   AASPAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Savolainen, V.
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Cutler, C.P.
                                                                                                                                    Vertebrata; Gnathostomata; Osteichthyes; Actinopterygii;
                                                                                                                                                                                             Anguilla anguilla
                                                                                                                                                                                                               European eel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Chlorophyta/Embryophyta
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                                   Unpublished
                                                                                           Elopomorpha; Anguilliformes; Anguilloidei; Anguillidae; Anguilla
                                                                                                                Actinopteri; Holostei; Halecostomi; Teleostei; Elopocephala;
                                                                                                                                                       Metazoa; Eumetazoa; Bilatería; Coelomata; Deuterostomia; Chordata;
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                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
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/product="ribulose-1,5-bisphosphate-carboxylase"
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/isolate="sample RA12"
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90.5%;
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Pred. No. 3.70e+00;
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Best Local Similarity 90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                vertebrate hedgehog homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g452159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-NOV-1993) to the EMBL/GenBank/DDBJ databases. C.P.
                                                                                                                                                                                                                                            Floor plate and motor neuron induction by vhh-1, a vertebrate
                                                                                                                                                                                                                                                                    Dodd, J
                                                                                                                                                                                                                                                                                                      Roelink, H., Augsburger, A., Heemskerk, J., Korzh, V., Norlin, S.,
                                                                                                                                                                                                                                                                                                                           Actinopterygii; Cypriniformes; 1 (bases 1 to 2600)
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Animalia; Chordata; Vertebrata; Osteichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                              zebrafish cDNA to mRNA.
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                                                                                                                                                                                                    homolog of hedgehog expressed by the notochord Cell 76 (4), 761-775 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     floor plate induction; motor neuron induction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                     Altaba, A., Tanabe, Y., Placzek, M., Edlund, T., Jessell, T.T.M.
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               /tissue_type="total embryo"
/tissue_lib="lambda ZAP-II"
320..388
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a 277 c 261 g 271 t
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CLAGIFIGTIQALLLTINDFKPVYQDRVAPPGLSHTPRSEKSEMSFKVGDPSTYQKYV
KAWHDFLQAYNDSKQEMMMKYEDCGDTPKSYINRGELDNNQGIKKACIFRRSWLDKCS
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97..1008
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1116..>1147
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                                                                           /sequenced_mol="cDNA to mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /EC_number="3.6.1.37"
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/gene="vhh-1"
                                                                                                  /dev_stage="9-16 hours post fertilization"
                                                                                                                     /organism="Brachydanio rerio"
                                                                                                                                            1..2600
                                                                                                                                                             Location/Qualifiers
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Pred. No. 3.70e+00;
"'ematches 2;
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Best Local Similarity 87.0%;
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4p16.3.
                                                L30G1 is from cosmid library LA04NC01 constructed at the Human Genome Center, Los Alamos National Laboratory, NM 87545 under the auspices of the U.S. Department of Energy. The library was constructed using flow-sorted human chromosome 4 from a
                                                                                                                                                                                                                                                                                            An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-JAN-1996) Sanger Centre, Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DNA sequence from cosmid L30G1, Huntington's Disease Region,
                                                                                                                                                                                    The true left end of clone L30Gl is at 1 in this sequence. The true right end of clone L26El2 is at 21857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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chromosomes 4, 8 and 21.
                    Hamster-Human hybrid cell line ( UV20HL21-27 )
                                                                                                                                                                                                                                                                sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                          has been finished according to sequence map criteria as follows.
                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the entire insert of clone L30G1. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB10 1RQ, England. E-mail enquires: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heathcott,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                          The true right end of clone L30G1 is at 35473.
                                                                                                                                                                                                                                            eature key.
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/codon_start=1
/db_xref="PID:g452160"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSTEDLHTMTAAYASSVRAGQKVMVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPGDKVLAADSAGNLVFSDF IMFTDRDSTTRRVFYVIETQEPVEKITLTAAHLLFVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSRLAVEAGFDWVYYESKAH IHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDL
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Pred. No. 3.70e+00;
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                      containing human
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FEATURES misc\_feature misc\_feature misc\_feature repeat\_region repeat\_region source misc\_feature repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region misc\_feature repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region :epeat\_region 2Mb which is described in Baxendale et al, Nature Genetics 4 ( 1993 L30G1 is contained in a clone contig spanning /note="Alu 2532..2824 /note="Alu repeat: matches
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11991..12281 /note="Alu repeat: matches 1..112 of consensus"
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5638..6154 5085..5382 4618..4697 /note="Alu repeat: matches 308..1 of consensus"
4331..4708 /note="match: multiple ESTs"
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repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region		repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region
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es 1118 of consensus"	ss 3061 of consensus"	ss 3081 of consensus"	s 159308 of consensus"	s 831 of consensus"	ss 308240 of consensus"	ss 1306 of consensus"	83 % conserved"	s 30888 of consensus"	s 123308 of consensus"	e 1308 of consensus"	1155 of	s 3081 of consensus"	s 3081 of consensus"	s 270308 of consensus"	s 145185 of consensus"	s 1308 of consensus"	s 81148 of consensus"	s 161 of consensus"	s 245308 of consensus"	ss 1246 of consensus"	s 1308 of consensus"	3081 of consensus

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Note: remainder of annotations omitted.

ငှ Db 32887 agcctggatggtcccaatg 32905 Query Match 60.7%; Best Local Similarity 94.7%; Matches 18; Conservative 28 AGCCAGGATGGTCCCAATG 10 Score 17; DB 54; Length 35473; Pred. No. 3.70e+00; 0; Mismatches 1; Indels 0 Indels 0; Gaps 0

IDCUS HUMTCRB 684973 bp DNA PRI 14-JAN-1995
DEFINITION Homo sapiens (clones: K41A, K35, K26, K56, X21B, G54, H137, H18, H18/G15gap, G15, X1A, A27, A212, A14, H7.1, H12.18, H130, A16, C215, G1, C68, C21, X11, X6A, CBC1, CBC1/C29gap, and C29) germline
T-cc1 receptor beta chain, complete gene. KEYWORDS ACCESSION RESULT 12 C-beta gene segment; C-region; D-region; J-beta gene segment; J-segment; T cell receptor beta chain; TCR-beta gene; V-beta gene segment; V-segment; cell membrane protein; L36092 constant region; diversity region; germline; joining segment; trypsin; trypsinogen; variable segment. g540583

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SOURCE REFERENCE FEATURES REFERENCE AUTHORS TITLE TITLE ORGANISM MEDLINE JOURNAL JOURNAL AUTHORS source source repeat\_unit repeat\_unit repeat\_unit repeat\_unit repeat\_unit repeat\_unit repeat\_unit Slightom, J.L., Siemieniak, D.R., Sieu, L.C., Koop, B.F. and Hood, L. Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell Homo sapiens A72B3) DNA; Homo sapiens (clone library: Kai Wang's) DNA; Homo sapiens (clone library: Kai Wang's) (tissue library: ATCC 1521) DNA; Homo sapiens (clone library: Kai Wang's) DNA; Homo sapiens (DNA; Homo sapiens) DNA; Homo sapiens library: Kai Wang's) DNA; Homo sapiens (clone library: YAC 234 A6F6) DNA; Homo sapiens (clone library: YAC 234 A6F6) DNA; Homo sapiens (clone library: YAC 234 A6F6) DNA; Homo sapiens (clone library: YAC 234 A72B3) DNA; Homo sapiens (clone library: Kai Wang's) DNA; Homo sapiens (clone library: Kai Wang's) DNA; Homo sapiens (clone library: YAC D49H4) DNA; Homo sapiens (clone library: YAC D49H4) DNA; Homo sapiens (clone library: YAC D49H4) DNA; Homo sapiens (clone library: Kai Wang's) (tissue library: ATCC 1521) DNA; Homo sapiens (clone library: Kai Wang's) (tissue library: ATCC 1521) DNA; Homo sapiens Colone sapiens Colone sapiens DNA; Homo sapiens (clone sapiens Colone sa Rowen, L., Koop, B.F. and Hood, L. 94292194 Genomics 20 (2), 149-168 (1994) receptor gene locus: direct primer-walking using cosmid template Unpublished (1994) Sequence of the human T cell receptor beta locus Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; library: YAC 199 B157G9) DNA; Homo sapiens (clone library: YAC 234 Homo sapiens (clone library: YAC D49H4) DNA; Homo sapiens (clone (bases 368065 to 442094) (bases 1 to 684973) /rpt\_family="Alu" 8317..8427 /rpt\_family="Alu" complement (23629..23893) /note="putative" /rpt\_family="Alu" 2429..2988 /organism="Homo sapiens"
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Query Match

60.7%;

Score 17;

DB 61;

Length 684973;

annotations omitted.

REFERENCE AUTHORS TITLE SOURCE ORGANISM 受用日日の日 RESULT Ş Ş ORIGIN BASE COUNT FEATURES COMMENT REFERENCE KEYWORDS ACCESSION DEFINITION RESULT Db 523902 attgggaccatcctggc 523918 Query Match 57.1%; Best Local Similarity 94.4%; Matches Matches JOURNAL TITLE AUTHORS Best Local X91841; 05-0CT-1995 (Rel. 45, Created) 22-APR-1996 (Rel. 47, Last updated, Version 5) H.sapiens DNA loop attachment sequence (clone LASO5) Alu sequence; loop attachment sequence. misc\_feature source HSLAS05SQ standard; DNA; PRI; 326 BP repeat\_region 11 ATTGGGACCATCCTGGC 27 11 ATTGGGACCATCCTGGCT 28 29 attgagaccatcctggct 46 13 = = = = = Jackson, D.A., Bartlett, J.M. and Cook, P.R. Sequence attaching loops of nuclear and mitochondrial DNA to underlying structures in human cells: the role of transcription Eukaryotae; | Vertebrata; H.sapiens DNA loop attachment sequence (clone LAS05).  $\times 10^{-10}$ Related sequence: Submitted (25-SEP-1995) P.R. Cook, Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE, Direct Submission Cook, P.R. Homo sapiens J.Jurka, Proc.Natl.Acad.Sci.USA, 85, 4775-4778, 1988. Nucleic Acids Res. 24, 1212-1219 (1996) Alu sequence; loop attachment sequence g1009421 HSLAS05sQ NCBI gi: 1009421 1 (bases 1 to 326) human. Similarity 100.0%; 17; Conservative (bases 1 to 326) 118 a Conservative /note="DNA loop attachment sequences" 1 72 c 80 g 56 t /rpt\_family="Alu" <1..>326 /clone lib="DNA loop attachment sequences (LAS)"
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Homo sapiens (human)

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

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                                                                                                                                                                                                                                      NID
                                                                                                                 REFERENCE
                                                                                                                                                                           SOURCE
                                                                                                                                                                                           SEGMENT
                                                                                                                                                                                                                                                                                              POCOS
                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                               DEFINITION
JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.1%; Score 16; DB 9; L
Best Local Similarity 94.4%; Pred. No. 1.76e+01;
Matches 17; Conservative 0; Mismatches 1
                                                                                                   AUTHORS
                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Alu"
Sequence 326 BP; 118 A; 72 C; 80 G; 56 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                         11 ATTGGGACCATCCTGGCT 28
                                                                                                                                                                                                                                                                                                                                                                       29 attgagaccatcctggct 46
         Mutant U5A cells are complemented by an interferon-alpha beta receptor subunit generated by alternative processing of a new member of a cytokine receptor gene cluster EMBO J. 14 (20), 5100-5108 (1995)
                                                                                                                                                                                        hematopoietin receptor family; interferon receptor. 4 of \boldsymbol{8}
                                                                                                                                                                                                                                                  L42240
                                                                                                                                                                                                                                                                            HUMIFNAM04 877 bp DNA PRI 04-APR-1996
Homo sapiens (clone Q-20D3) interferon receptor (IFNAR2) gene, exon
                                                                                                                                                                                                                                   g994719
                                                                                 Lutfalla,G., Holland,S.J., Cinato,E., Monneron,D.,
Rogers,N.C., Smith,J.M., Stark,G.R., Gardiner,K., I
                                                                                                                                                            Homo sapiens
                                                                                                                                                                         Homo sapiens (clone: Q-20D3) (clone library: LL21NCO2-Q) DNA.
                                                                                                                                                                                                                    cytokine receptor; helical cytokine receptor family;
 96067138
                                                                     Kerr, I.M. and Uze, G.
                                                                                                                            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                              (bases 1 to 877)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="48 nucleotide number" <1..>326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="DNA loop attachment sequences"
                                                                                                                                                                                                                                                                                        877 bp
                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 326;
                                                                                 Mogensen, K.E.,
                                                                                                   Reboul, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                       BASE COUNT
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                                                               Query Match 57.1%;
Best Local Similarity 94.4%;
                                                     Matches
                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                              exon
              145 agccaggatggtctcaat 162
 28
  AGCCAGGATGGTCCCAAT 11
                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                         NCBI gi:
                                                                                                                       237 a
                                                    Conservative
                                                                                                                      /number=5
a 212 c
                                                                                                                                                                      /number=5
582..754
                                                                                                                                                                                                                                                                                /clone_lib="LL21NCO2-Q"
/map="721q22.1"
order(L42239:1569..1661,1..581)
                                                                                                                                                                                                                             582..754
                                                                                                                                              /gene="IFNAR2"
/note="encodes SD100A s3-s7"
                                                                                                                                                                                                  /note="encodes SD100A s3-s7"
                                                                                                                                                                                                               /gene="IFNAR2"
                                                                                                                                                                                                                                          /number=4
                                                                                                                                                                                                                                                        /note="1.6 kB"
                                                                                                                                                                                                                                                                                                                         /clone="Q-20D3"
                                                                                                                                                                                                                                                                                                                                      /macronuclear
                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                     /partial
                                                               Score 16; DB 90; Length 877; Pred. No. 1.76e+01;
                                                                                                                    200 g
                                                    0; Mismatches
                                                                                                                      228 t
                                                     1; Indels
                                                    0;
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Jackson D.A., Bartlett J.M., Cook P.R.;
"Sequence attaching loops of nuclear and mitochondrial DNA to underlying structures in human cells: the role of transcription

source

/cell\_line="Rela"
/clone\_lib="NNA loop attachment sequences (LAS)"
/clone="LAS05"

/organism="Homo sapiens"

J.Jurka, Proc.Natl.Acad.Sci.USA, 85, 4775-4778, 1988

Location/Qualifiers

Related sequence:

Nucleic Acids Res. 24:1212-1219(1996).

units";

1-326

Submitted (25-SEP-1995) to the EMBL/GenBank/DDBJ databases. P.R. Cook, Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OXI 3RE, UK

Cook P.R.;

1-326

Search completed: Tue Mar 25 02:47:15 1997 Job time : 63 secs.

Gaps

0;

\*

US-08-644-289-4 mg

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:52:36 1997; MasPar time 9.33 Seconds 280.530 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-08-644-289-4 (1-30) from US08644289.seq 30

N.A. Sequence: Сотр: 1 AGTCGGATCCTGGAGTGAGCCCTGCTGTCT 30 TCAGCCTAGGACCTCACTCGGGACGACAGA

Scoring table: TABLE default Gap 10

Nmatch STD: Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.779; Variance 3.522; scale 1.641

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	t . Score	Query Match	Length DB	B	ID	Description	Pred. No
O	1 24	80.0	91	9	Q51746	Oligonucleotide probe	
O	2 21	70.0		12	Q67883	Murine p53 DNA.	
	3 20	66.7		9	Q51746	Oligonucleotide probe	
	4 19	63.3		21	T10488	Human wild-type p53 g	
o 	5 17	56.7		11	Q62363	Fragment coding for h	
o	6 17	56.7		Ξ	Q62361	Fragment coding for h	3.91e+00
<u>ه</u>	7 17	56.7	1062	Ξ	Q62359	Fragment coding for h	
0	8 17	56.7	1173	5	Q29632	Hepatitis C virus HC-	

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44 45	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9
15 15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	16	16	16	16	16	17	17	17	17	17	17	17
50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	53.3	53.3	53.3	53.3	53.3	56.7	56.7	56.7	56.7	56.7	56.7	56.7
9416 12001	9400	9379	9185	9185	8316	7350	7310	7310	6905	4757	4337	2793	1847	1191	1180	1173	854	504	456	456	450	438	274	3017	435	435	71	71	9502	1512	1483	1182	1182	1182	1181
13 3	ω	6	ш	2	<b>-</b>	17	20		_	17	14	21		14	14	7		22	_	-	18	22	<u>,</u>	_	13	13	13	13	13	12	12	w	12	22	15
Q22871 Q76213	Q21744	Q36209	Q05956	Q10566	Q05955	Q98955	Q98221	N90336	N92103	Q98957	Q82833	T16372	N90719	Q79142	Q79144	Q43893	Q03296	T34163	N90331	N92101	T19056	T34165	N92102	Q05271	Q80363	Q80434	Q80676	Q80398	Q74770	Q67863	Q67864	Q22995	Q67884	T29719	Q97854
NANBV Hutch c59 isola HSV L/ST region.	Compiled HCV cDNA.	site cDNA for F	Sense strand of the c	C virus	C virus	Complete B-G gene enc		Composite hepatitis C	Combined open reading	Chicken genomic DNA f	Human stromalin-1 DNA	Obesity protein codin	ĕ	C	Hepatitis C virus gen	NANB hepatitis virus	Sequence of clone cZ1	Mouse ob cDNA clone p	Hepatitis C virus (HC	Sequence of the hepat	gei		Sequence of the hepat		Humanized antibody L2	CDR-grafted L243-gH V	embly óli	L243-c	C				DNA		Human p53 cDNA.
3.79e+01 3.79e+01				3.79e+01			٠.	•	•	3.79e+01	•					3.79e+01		3.79e+01	•	•		-	3.79e+01		1.24e+01	1.24e+01	1.24e+01	•	٠	-	•			•	3.91e+00

### ALI GNMENTS

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be useful as an initial screen for mycobacterial infection.	cross reacted to a few non-mycobacterial spp. The probe may	(Q51735). It hybridized to all spp. of mycobacteria tested, but	Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14	Claim 3; Page 14; 23pp; English.	samples	detection and amplification of Mycobacteria nucleic acid in	New oligo:nucleotide probes specific for Mycobacteria - used for	WPI; 93-378844/48.	Shank DD, Spears PA;	(BECT ) BECTON DICKINSON CO.	26-MAY-1992; US-889651.	24-MAY-1993; 108325.	01-DEC-1993.	EP-571911-A.	Synthetic.	88.	Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;	Oligonucleotide probe MK14-A	31-MAY-1994 (first entry)	Q51746;	Q51746 standard; cDNA; 91 BP.	

30 AGACAGCAGGGCTCACTCCAG

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RESULT PROCESS OF PROC
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                            1071 agacagcagggctcactccag 1091
                                                                                                                                                                                                                                                                                                                                  between this donor plasmid and AIVAC rescuing virus produced recombinant virus vCP263, which contains the vaccinia H6 promoted murine p53 in the
                                                                                                                                                                                                                                                                                                                                                                                         bp fragment contains a BamHI site followed by H6 promoted p53. This was inserted into pNC5LSP5 to generate plasmid pMM148 containing H6 promoted wildtype murine p53 in the ALVAC C5 insertion locus. Recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the p53 gene, and the 5' end overlaps fragment II. products were pooled and primed with MM080 and MM085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as a template. The 228 bp amplified fragment contains the H6 promoter and the 5'-most bases of the murine p53 gene. Fragment II was produced using primers MM082 and MM083 and plasmid p11-4 as a template. The 129 bp amplified fragment contains the 3' end of the H6 promoter, the 5'-most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used in the construction of an ALVAC-based recombinant virus containing the wild-type murine p53 gene. Three PCR fragments were generated. Fragment I was produced using primers MMO80 and MMO81 and plasmid pRW825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also Q51735-45
Sequence 91 BP;
                                                                                                                                                                                                                                                                         an antigenic or immunological response,
                                                                                                                                                                                                                                                                                                           C5 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pli-4 as a template.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fragment III was produced using primers MM084 and MM085 and plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q67883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q67883 standard;
                                                                                                                                                                                                                                                  pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bases of the murine p53 gene, and 15 bp which overlap fragment III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation initiation codon to the stop codon. This sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the wildtype murine p53 gene from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 31; Fig 38; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding cytokine and/or tumour associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Attenuated recombinant virus used for cancer therapy - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 94-263767/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1994; U00888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9416716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogen; human; interferon; IFN; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymerase chain reaction; poxvirus; pSD542; immunological response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine p53 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1995 (first entry)
                                                                                                                   y Match 70.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
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Paoletti E, Tartaglia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                  1173 BP;
                                                                                                                                                                                                                                                                                                      The resulting virus may be used in a composition for inducing
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The 301 bp amplified fragment contains the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   951747-59.
A; 17 C;
                                                                                                                                                                                                               279 A;
                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽₽
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Pred. No. 6.72e-04;
                                                                                         0;
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                                                                                         Mismatches
                                                                                                                                                                                                               349 C;
                                                                                                                   21; DB 12;
No. 3.08e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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                                                                                                                                                                                                                  304
                                                                                                                                                                                                                                                                            for immunisation against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                         0;
                                                                                                                                                Length 1173;
                                                                                                                                                                                                               ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                         Indels
                                                                                                                                                                                                               241 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The resultant 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The three PCR
                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                   Gaps
                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1993
24-BAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q51746
Q51746;
create antibodies directed against this sequence in an alternatively spliced p53. The antibodies are useful in the diagnosis and prognosis of human cancer and in the study of p53 and alternatively spliced p53
                                               gene. An epitope from intron 10 of the human p53 gene is used to
                                                               N-terminal (nucleotides -111 to 1090) portion of the wild-type p53
                                                                                                                                                                                                                                                                                                    Tumour suppressor; p53; alternative splicing; antibody; cancer; proliferative disorder; psoriasis; prognosis; diagnosis; cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                              T10486-T10488 are primers used in a RT-PCR reaction to obtain an
                                                                                             Disclosure; Page 7; 40pp; English.
                                                                                                                            useful in diagnosis or prognosis of cancer,
                                                                                                                                           New antibodies specific for alternatively spliced mammalian p53
                                                                                                                                                             WPI; 96-140137/15.
                                                                                                                                                                           Kulesz-Martin MF;
                                                                                                                                                                                         14-JUN-1994; US-259612. (HEAL-) HEALTH RES INC.
                                                                                                                                                                                                                         05-JUN-1995;
                                                                                                                                                                                                                                                        CA2150994-A.
                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                      reverse transcriptase polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                     Tumour suppressor; p53; alternative splicing;
                                                                                                                                                                                                                                                                                                                                 Human wild-type p53 gene
                                                                                                                                                                                                                                                                                                                                                   03-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                      T10488;
                                                                                                                                                                                                                                                                                                                                                                                      T10488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be useful as an initial screen for mycobacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cross reacted to a few non-mycobacterial spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Q51735).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide probe MK14-A consists of nucleotides 5-95 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 14; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP-571911-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1994 (first entry)
                                                                                                               individual treatment regimes.
                                                                                                                                                                                                                                       5-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 hsvhhvvhhvhvsvvvvhhvvhvvhhvhyh 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGTCGGATCCTGGAGTGAGCCCTGCTGTCT 30
                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          It hybridized to all spp. of mycobacteria tested,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                    N-terminal antisense RT-PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 9;
Pred. No. 1.07e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 G;
                                                                                                                            and for establishing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The probe may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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US-08-644-289-4 mg

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RESULT
ID Q6
AC Q6
DT 18
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Best Local Similarity 100.0%;
                                                                                                                                         Matches
                                                                                                                                                     Best Local Similarity 100.0%;
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                        Non-radioactive detection of p53 specific antibodies - by capture on immobilised p53 or its fragments, then reaction with labelled second antibody, for diagnosis of tumours and suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 5
Q62363
Q62363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (p53as) and their expression. When the antibodies are injected into cells they may cause cell cycle arrest. Vectors contq. p53as cDNA may be used in gene therapy of cancers and other proliferative disorders
                         Q62361 standard;
                                                                                                                                                                                           each of these fragments.
Sequence 471 BP; 128 A;
                                                                                                                                                                                                                                                                                                                                                                               Klein R, Schranz P, Tessmer C, WPI; 94-135732/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fragment coding for human p53 amino acids 237-393. Human nuclear phosphoprotein p53; tumour suppressor gene product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. psoriasis.
             Q62361;
                                                                                                                                                                                                                       region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or 386-386. See Q62357-Q62366 for nucleic acid sequences coding for
                                                                                                                                                                                                                                                                  fragments of the p53 gene product containing the antibody-binding
                                                                                                                                                                                                                                                                               Antibodies specific for p53 are detected by binding to immobilised
                                                                                                                                                                                                                                                                                             Claim 13; Page 25; 35pp; German.
                                                                                                                                                                                                                                                                                                            screening
                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R51878.
                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1993; E02666.
30-SEP-1992; DE-232823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09408241-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contain start or stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= p53(237-393)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-oncogene;
18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_except= pos:109..111,aa:Arg
/note= *partial CDS, therefore sequence does not
                                                                                               376 agcagggctcactccag 392
                                                                                                                                                                                                                                                                                                                                                                                                              (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l8-NOV-1994 (first entry)
                                                                                  26 AGCAGGGCTCACTCCAG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 agtcggatcctggagtgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCGGATCCTGGAGTGAG 19
                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 BP;
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; tumour; antibody binding region; epitope;
                          cDNA; 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA; 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 A;
                                                                                                                                                                    56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
                           ₽₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В₽
                                                                                                                                                    Score 17; DB 11;
Pred. No. 3.91e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.63e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
C;
                                                                                                                                        0
                                                                                                                                                                                             133 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Volkmann M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                 DB 11; Length 471;
                                                                                                                                                                                              132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 T;
                                                                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                               Zentgraf H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                         Indels
                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                        Gaps
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           each of these Iraymore 984 BP;
           (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.
Klein R, Schranz P, Tessmer C, Volkmann M,
WPI; 94-135732/16.
                                                                                                                                                                                                                                   Fragment coding for human p53 amino acids 40-393. Human nuclear phosphoprotein p53; tumour suppressor gene product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or 368-386. See Q62357-Q62366 for nucleic acid sequences coding for
                                                     30-SEP-1992;
                                                                                               WO9408241-A.
                                                                                                            contain start or stop codons"
                                                                                                                        /product= p53(40-393)
/transl_except= pos:700..702, aa:Arg
/note= "partial CDS, therefore sequence
                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                       anti-oncogene; cancer; tumour; antibody binding region; epitope; ds.
                                                                                                                                                                                                                                                                                           Q62359 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies specific for p53 are detected by binding to immobilised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 24; 35pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         second antibody, for diagnosis of tumours and suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on immobilised p53 or its fragments, then reaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-radioactive detection of p53 specific antibodies - by capture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; R51876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein R, Schranz P, Tessmer C, WPI; 94-135732/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9408241-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contain start or stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_except= pos:622..624, aa:Arg
/note= *partial CDS, therefore sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-oncogene; cancer; tumour; antibody binding region; epitope; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nuclear phosphoprotein p53; tumour suppressor gene product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fragment coding for human p53 amino acids 66-393.
                                                                  30-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragments of the p53 gene product containing the antibody-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1993;
                                                                                 14-APR-1994.
                                                                                                                                                                                                                                                                l8-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             889 agcagggctcactccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= p53(66-393)
                                                                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                    AGCAGGGCTCACTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                 26232
e fragments.
224 A;
                                                     DE-232823.
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                Location/Qualifiers 1..1062
                                                                                                                                                                                                                                                                                           cDNA; 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               905
                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                         ۰,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 C;
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Volkmann M,
                                                                                                                                                                                                                                                                                                                                                                                                                        17; DB 11;
No. 3.91e+00;
                                                                                                                           does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 G;
                                                                                                                           not
                                                                                                                                                                                                                                                                                                                                                                                                         0.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 984;
                          Zentgraf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zentgraf H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       labelled
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Claim 13; Page 22; 35pp; German.

screening

region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or Antibodies specific for p53 are detected by binding to immobilised fragments of the p53 gene product containing the antibody-binding

See Q62357-Q62366 for nucleic acid sequences coding for

Query Match Best Local S

Match 56.7%; Local Similarity 100.0%; les 17; Conservative

<u>,</u>

Mismatches

0;

Indels

0; Gaps

<u>.</u>

Score 17; DB 11; Length 1062; Pred. No. 3.91e+00;

Sequence

1062 BP;

246 A;

329 C;

279 G;

208 T;

each of these fragments.

368-386.

Matches

Non-radioactive detection of p53 specific antibodies — b on immobilised p53 or its fragments, then reaction with

by capture labelled

second antibody, for diagnosis of tumours and suitable for

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RESULT RE
   RESULT
ID QS
AC QS
DT OF
DE HI
KW UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     င့
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                                                                                                                                                                                                                                                                                                           မှ
                                                                                                                                                                                                                                                                                                                                                                              문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.7%;
Best Local Similarity 90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
   Ubiquitin-conjugating enzyme; p53 protein; cell cycle; cell proliferation; cancer; psoriasis; fibrosis; ds.
                                                                                                                                                                         Q97854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligo-nucleotide primers with nucleotide sequences corresp. to part. of the viral RNA Disclosure; Page 27; 54pp; English. This sequence represents the 3' region of hepatitis C virus RNA. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; primer; polymerase chain reaction; ss. Hepatitis C virus. EP-510952-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-1993 (first entry)
Hepatitis C virus HC-J1 3' region.
Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q29632;
                                                            Human p53 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1992; 303625.
26-APR-1991; JP-191376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 8
Q29632 standard; DNA; 1173
                                                                                                  06-DEC-1995
                                                                                                                                      Q97854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was isolated from several samples and homology compared, and the respective sequence of about 1900-2500\ \mathrm{nucleotides} of the 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       original sample was obtained from human and chimpanzee plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of non-A, non-B hepatitis virus - using new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 92-359137/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamura T, Okamoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-0CT-1992.
                                                                                                                                                                                                                                                                                                                                        516 agacagcaaggcacactccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMO ) IMMUNO JAPAN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        967 agcagggctcactccag
                                                                                                                                                                                                                                                                                                           30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 AGCAGGGCTCACTCCAG
                                                                                                                                                                                                         9
proliferation; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                           AGACAGCAGGGCTCACTCCAG
                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and 1100 nucleotides of the 3' terminus determined.

1173 BP; 248 A; 348 C; 305 G; 272 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                  (first entry)
                                                                                                                                                                     cDNA; 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
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                                                                                                                                                                                                                                                                                                                                                                           536
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                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.91e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1173;
                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.7%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1084 agcagggctcactccag 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-1994;
27-MAY-1994;
p-PSDB; R91933.
Use of wild-type p53 gene — in a medicament for suppressing the neoplastic phenotype of a cancer cell lacking wild-type p53 prot Claim 1; Page 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant p53 in Sf9 insect cells for use as a component of an in vitro ubiquitin conjugating system.

Sequence 1181 BP; 275 A; 366 C; 306 G; 234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle regulatory proteins - also new ubiquitin conjugating enzymes, their related nucleic acid, vectors, antibodies etc., useful for regulating
                                                         Chen P, Lee W; WPI; 96-223439/23.
                                                                                                    24-AUG-1990;
                                                                                                                                08-MAY-1996.
                                                                                                                                            /transl_except=
EP-710722-A1.
                                                                                                                                                                                    /product= p53 protein.
misc_difference 19..21
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                        bladder cells; prostate carcinoma cell;
                                                                                                                                                                                                                                                                                                    osteosarcoma cells; lung carcinoma cells; lymphoma cells;
                                                                                                                                                                                                                                                                                                                 p53 gene; cancer; carcinoma; neoplastic; neoplasia; phenotype;
                                                                                                                                                                                                                                                                                                                                Wild type p53 gene sequence.
                                                                                                                                                                                                                                                                                                                                                29-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                           T29719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was subcloned into a baculovirus vector for expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human p53 cDNA (given in Q97854) was amplified from a HeLa cell cDNA library using the primers given in Q97852-53. The gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g. cell proliferation
Disclosure; Page 105-106; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; R79658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 95-255137/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cottarel G, Draetta G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09518974-A.
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                                                                                                                 23-AUG-1991;
                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                       leukaemia cells; soft tissue sarcoma cells; breast cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-1994; US-305520
                                                                                    (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    26 AGCAGGGCTCACTCCAG 10
                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 1182 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-176937.
US-247904.
US-250795.
                                                                                                    US-573405
                                                                                                                  307791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                        CAT encodes
                                                                                                                                                                                                                               1..1182
                                                                                                                                                                                                                                               Location/Qualifiers
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1..1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eckstein JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17; DB 15;
Pred. No. 3.91e+00;
                                                                                                                                                        Aspartic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gyuris J,
                                                                                                                                                                                                                                                                           ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The gene
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                protein
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RESULTING A CONTROL OF STATE O ន្តន្តន្តន្តន င 밁 Best Local Similarity 100.0%; Query Match Matches Query Match 56.7%; Best Local Similarity 100.0%; Matches mutant p53 gene was obtained from plasmid Cx22A and cloned into pMM110 to generate pMM143. Recombination between pMM143 and ALVAC rescuing virus produced recombinant virus vCP270, which contains the vaccinia H6 promoted mutated human p53 in the C5 locus. The resulting virus may be used in a composition for inducing an antigenic or immunological murine; interleukin-2; II-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector; plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response; polymerase chain reaction; poxvirus; pSD542; immunological response; The wild-type p53 gene can be used in the production of a medicament for suppressing the neoplastic phenotype of a cancer cell lacking endogenous wild type p53 protein. Cancer cells suppressed in such fashion include osteosarcoma cells, lung carcinoma cells, lymphoma cells, leukaemia cells, soft tissue sarcoma cells or breast, bladder Cox WI, Paoletti WPI; 94-263767/32. 21-JAN-1994; U00888. 21-JAN-1993; US-007115. Q67884 standard; DNA; 1182 Sequence response, ie. for immunisation against pathogens. Sequence 1182 BP; 276 A; 365 C; 307 G; The plasmid pMM110 (see also Q67864) contains the vaccinia H6 promoter and the wild type human p53 gene in the ALVAC C5 insertion site. The position 524, changing an Arg residue at position 175 to a His residue construction of an ALVAC-based recombinant virus containing a mutant This sequence represents the wildtype human p53 gene from the translation initiation codon to the stop codon. This sequence was used in the DNA encoding cytokine and/or tumour associated antigen Example 32; Fig 39; 232pp; English. Attenuated recombinant virus used for cancer therapy - comprises 19-JAN-1994; US-184009. 04-AUG-1994. W09416716-A. Synthetic. pathogen; human; interferon; IFN; ss. Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; Human p53 DNA. 23-MAR-1995 067884; or prostate carcinoma cells. form of the human p53 gene. The mutant form has a G>A substitution at (VIRO-) VIROGENETICS CORP. Paoletti E, Tartaglia J; 1182 BP; Conservative Conservative (first entry) 56.7%; 278 A; ₽P Score 17; DB 22; Pred. No. 3.91e+00; Pred. No. 3.91e+00; Score 17; 9 0; Mismatches Mismatches 366 C; DB 12; 304 G; 0; Indels <u>,</u> Length 1182; Length 1182; Indels 234 T; 234 T; 0: 0; Gaps Gaps 0 <u>,</u>

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Matches Best Local 1084 ageagggeteactecag 1100 Vaccinia H6 promoter/human p53 expression cassette from vCP207.
Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; p53; wild type; mutant; p53\*tXbaISp6/T3; p53-21XbaI; p53-238XbaI; is replaced by 273 His, a mutation found exclusively in tumour cells. Sequence 1182 BP; 277 A; 368 C; 303 G; 234 T; colon carcinoma, lymphoma, leukaemia, etc., suggesting that mutation of the p53 genes is involved in oncogenesis. Specifically 273 Arg Q22995; 23-JUL-1992 (first entry) Sequence encoding 53 kD cellular protein. /note= "Flanking sequence" /product= Wild type human p53 misc\_feature 1415..1483 /note= "Vaccinia H6 promoter"
CDS 233..1414 /\*tag= /note= "Flanking sequence" promoter 109..232 misc\_feature pathogen; ss. ALVAC (CPpp) p53; vaccinia; H6 promoter; plasmid; pRW825; expression cassette; Q67864; Q67864 standard; DNA; 1483 BP genes. Variant forms of p53 are found in human breast, cancers caused by defective, mutant or absent cancer suppressor p53 cDNA, or its gene prods., can be used to suppress and eradicate Claim 5; Page 15; 25pp; English. neoplastic phenotype e.g. in osteo-sarcuma(s), leukaemia(s), Cloned p53 cDNA and protein prods. - for suppression of WPI; 92-090221/12. Lee WH, Chen PL; 24-AUG-1990; US-573405. EP-475623-A. Homo sapiens Cancer therapy; cancer suppressor gene; oncogenesis; ss Q22995 standard; DNA; 1182 WO9416716-A. /\*tag= Synthetic. 22-MAR-1995 (first entry) P-PSDB; R22238. (REGC ) UNIV OF CALIFORNIA. 23-AUG-1991; 18-MAR-1992. /\*tag= lymphoma(s), etc. 26 AGCAGGGCTCACTCCAG 10 Similarity 100.0%; Conservative 307791. poxvirus; antigenic response; immunological response; 1..108 Location/Qualifiers Location/Qualifiers 56.7%; BP. Score 17; DB 3; I Pred. No. 3.91e+00; <u>,</u>, Mismatches Length 1182; 0; Indels lung or 0; Gaps 0

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Best Local Similarity 100.0%;
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21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
(VIRO-) VIROGENETICS CORP.
Cox WI, Paoletti E, Tartaglia J;
WPI; 94-263767/32.
               04-AUG-1994.
21-JAN-1994; U00888.
21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1316 agcagggctcactccag 1332
                                                                                                                                                                                                                                                                                                                                                                       Vaccinia H6 promoter/human p53 expression cassette from vP1101.
Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; p53; wild type; mutant; p53wtXbaISP6/T3; p53-21XbaI; p53-238XbaI; vaccinia; H6 promoter; plasmid; pRW825; expression cassette;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q67863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutant genes were derived from plasmids p53wtXbaISP6/T3, p53-21XbaI are p53-238XbaI respectively. The vaccinia H6 promoter was derived from plasmid pRW825 and precisely linked to the 5'-most region of the p53 gene. The expression cassettes generated by linking the vaccinia H6 promoter and the p53 genes may be cloned in to the poxvirus insertion plasmid, ALVAC, to give vCP207, vCP193 and vCP191 recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding cytokine and/or tumour associated antigen Example 15; Fig 18; 232pp; English.
                                                                                  /note= "Flanking sequence" W09416716-A.
                                                                                                                  /*tag=
                                                                                                                                     misc_teature
                                                                                                                                                                                        Sg
                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                         misc feature
                                                                                                                                                                                                                                                                                                                                                         ALVAC (CPpp) p53; poxvirus; antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q67863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viruses may be used in a composition for inducing an antigenic or immunological response, ie. for immunisation against pathogens. Sequence 1483 BP; 367 A; 415 C; 372 G; 329 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viruses, and into NYVAC to give vP1101, vP1096 and vP1098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mutant forms of the human p53 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         construction of poxvirus based recombinant viruses expressing wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in vP1101 and vCP207, respectively. These sequences were used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            containing the vaccinia H6 promoter and the wild type human p53 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in Q67863-64 represent expression cassettes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Attenuated recombinant virus used for cancer therapy - comprises
                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                    /note= "Flanking
                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                         pathogen; ss.
 (VIRO-) VIROGENETICS CORP
                                                                                                                                                     /product= Human
                                                                                                                                                                       /*tag=
                                                                                                                                                                                                      /note= "Vaccinia
                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 AGCAGGGCTCACTCCAG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 1512
                                                                                                                                                                     o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                     a H6 promoter"
269..1450
                                                                                                                                       1451
                                                                                                                                                                                                                                     g sequence"
145..268
                                                                                                                                                  wildtype p53
                                                                                                                                                                                                                                                                                       1..144
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 12; Length 1483; Pred. No. 3.91e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                            response;
                                                                                                                                                                                                                                                                                                                                                          immunological response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The wild type and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
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                                                 Matches
                                                                 Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.7%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1352 agcagggctcactccag 1368
8794 agacagcaaggcacactccag
                                                                                                                                                                                  HCV genes and the corresponding proteins - used in the production of anti-HCV antibodies and the detection of HCV infection Claim 7; Pages 12-17; 35pp; Japanese. Q74770 encodes R66995 the HC-J1/protein, the cDNA can be used in the construction of an expression vector for the transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid, ALVAC, to give vCP207, vCP193 and vCP191 recombinant viruses, and into NYVAC to give vP1101, vP1096 and vP1098. The viruses may be used in a composition for inducing an antigenic immunological response, ie. for immunisation against pathogens. Sequence 1512 BP; 379 A; 419 C; 380 G; 334 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding cytokine and/or tumour associated antigen Example 15; Fig 17; 232pp; English.

The sequences given in Q67863-64 represent expression cassettes containing the vaccinia H6 promoter and the wild type human p53 gene in vPl101 and vCP207, respectively. These sequences were used in the construction of poxvirus based recombinant viruses expressing wild type
                                                                                                                                                                                                                                                                                                                                               11-OCT-1994.
10-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q74770
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus gene HC-J1/cDNA.
Hepatitis C virus; HCV gene HC-J1/cDNA; specific antibodies;
Hepatitis C virus.
                                                                                                                  and polyclonal HCV-specific antibodies. Sequence 9502 BP; 1879 A; 2847
                                                                                                                                                     of proteins and peptides, useful in the preparation of monoclona
                                                                                                                                                                     of a host cell. The host cell can then be used in the production
                                                                                                                                                                                                                                                                              P-PSDB; R66995.
                                                                                                                                                                                                                                                                                              WPI; 94-362594/45.
                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
J06284887-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q74770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter and the p53 genes may be cloned in to the poxvirus insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p53-238XbaI respectively. The vaccinia H6 promoter was derived from plasmid pRW825 and precisely linked to the 5'-most region of the p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mutant forms of the human p53 gene product. The wild type and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Attenuated recombinant virus used for cancer therapy -
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                                                                                                                                                                                                                                                                                                                                 10-DEC-1992; JP-360705
                                                                                                                                                                                                                                                                                                                (IMMO ) IMMUNO JAPAN KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; cDNA; 9502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                               Similarity
                                                 19;
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90.5%;
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                8814
                                                               Pred.
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                                                                                 Score 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 12;
                                               0;
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                                               Mismatches
                                                                 No. 3.91e+00;
                                                                                                                    2847 C;
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                                                                                                                     2691
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                                                                                 Length 9502;
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Search completed: Tue Mar 25 02:52:51 1997 Job time : 15 secs.

Mar 25 02:50

\* (ME)

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:51:15 1997; MasPar time 56.88 Seconds 434.390 Million cell updates/sec

Fabular output not generated.

Description: Title: >US-08-644-289-4 (1-30) from US08644289.seq

N.A. Sequence: Perfect Score: Comp: 30 1 AGTCGGATCCTGGAGTGAGCCCTGCTGTCT 30

TCAGCCTAGGACCTCACTCGGGACGACAGA

Scoring table: TABLE default

Gap 10

Nmatch STD: Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

embl-new5

genbank 94 1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI 10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database:

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7 23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5 30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2 37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLM1 43:PLM2 44:PLM3 45:PLM4 46:PLM5 47:PLM6 48:PLM7 49:PLM8 50:PR11 51:PR12 52:PR13 53:PR14 54:PR15 55:PR16 56:PR17 57:PR18 50:PR19 59:PR110 60:PR111 61:PR112 62:PR113 63:ROD1 64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8 71:STR 72:SYM 73:UMA 74:VRL1 75:VRL2 76:VRL3 77:VRL4 78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database:

genbank-new5 82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG 89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

Database:

u-embl46\_94 96:part1

RESULT 1
LOCUS
DEFINITION
ACCESSION

RATP53TS07

159 bp

DNA

14-JUL-1993

ALI GNMENTS

g205949

Rattus norvegicus tumor suppressor (p53) gene, exon 9. L07909 L07781

SOURCE SEGMENT KEYWORDS NID

ORGANISM

Rattus norvegicus tumor suppressor.

Rattus norvegicus (strain Sprague-Dawley) DNA.

Statistics: Mean 7.318; Variance 2.910; scale 2.515

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5.32e+00	Hepatitis C virus gen	HPCHCJ1	78	9502	56.7	17	45	G (
5 320+00		HSC17C	7 0	5000	56.7	17	<b>.</b> 5	2
	thymic stroma	HASTLSON	2 7	3127	56.7	17	42	
	mRNA fo	MUSTLSFB	83	3127	56.7	17	41	
5.32e+00	Mus musculus cytokine	MUSSDF1B	67	3127	56.7	17	40	
5.32e+00	sus monkey p53 mR	MACP53A	61	2184	56.7	17	39	G
.32e+0	lymph node mRNA	FCP53	9	2143	56.7	17	မ္တ	n i
	Cat lymph node mRNA f	CATP53	80 1	2143	56.7	17	37	ი ი
5 320+00	Human mBNA fragment f	1052501	5 O	3066	56.7	17	بر در	3 (
	7 E	HOMITON CE	0 0	1760	70.7	17	n n	3
5.320+00	pbs cellular t	HUMTROSH	2 2	1650	56.1	1 T	ر ا ا	O
٠	C virus,	HPCNS5J1	8	1224	56.7	17	32	G
	A for muta	HSP53002	54	1179	56.7	17	32	O
	mRNA for	HSP53009	54	1179	56.7	17	30	O
	mRNA for	HSP53007	54	1179	56.7	17	29	O
	mRNA for	HSP53003	54	1179	56.7	17	28	O
	mRNA for	HSP53008	54	1179	56.7	17	27	a
	mRNA for	HSP53004	54	1179	56.7	17	26	n i
	mRNA for	HSP 53011	54	1179	56.7	17	25 :	n n
5.32e+00	Human mRNA for mutate	HSP53005	54	1179	56.7		24	0 0
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5.32e+00	familiari	DOGP53MUT	3 3	844	56.7	17	21	C
•	sapiens ERCC2	HSXPDG1	9	54336	60.0	18	20	
•	ens ERCC2	HUMXPDG1	61	54336	60.0	18	19	
1.13e+00	p53 gene for	HSP53G	54	20303	60.0	18	18	O
1.13e+00	Rattus rattus trk pre	RATTRKPREC	69	2633	60.0	18	17	
1.13e+00	Human phosphoprotein	HUMP53A10	60	136	60.0	18	16	O
4.36e-02	va .	RNU07019	70	1273	66.7	20	15	0
8.05e-03	pseudogene fo	MMP53P	64	2132	70.0	21	14	0
8.05e-03		MUSP53PG	67	2130	70.0	21	ដ	0
8 056-03		MMD 53R	25	1773		21:	3:	<b>o</b> (
8 056-03	Monse p53 cellular tu	MIISP53M	67	1772	70.0	21 1	= 5	י כ
0.050-03	Pat mbul for mindlear	DVID 2.3	60	1627	70.0	2 :	10	, (
0520	norvegicus	RAIPSEUDO	3 9	1447	70.0	21 2		0
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.05e-0	p53 mRNA,	MUSP53B	6	1241	70.0	21	4.	O
.05e-0	ge	MMANT 10	చ	107	70.0	21	. w	O
1.43e-03	Mouse p53 mRNA, compl	MUSP53C	67	1322	73.3	22	2	O
1.43e-03	Rattus norvegicus tum	RATP53TS07	69	159		22	-	O
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Best Local Similarity 100.0%;
Matches 22; Conservative
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                                                                                                                                                                                different tissue types
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Mol. Cell. Biol. 6, 3232-3239 (1986)
                                                                                                                                                                                                                                                                                                                  Rotter, V.
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                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structure of the rat p53 tumor suppressor Nucleic Acids Res. 21, 713-717 (1993)
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                                                                                                                                                   92253421
                                                                                                                                                             Nucleic Acids Res. 20, 1979-1981 (1992)
                                                                                                                                                                                               Alternatively spliced p53 rRNA in transformed and normal cells
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                                                                                                                                                                                                                                                                                               Immunologically distinct p53 molecules generated by alternative
                                                                                                                                                                                                                                                                                                                                                               Eutheria; Rodentia; Myomorpha;
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/number=9
a 40 c
/gene="p53"
/map="11"
                                           /organism="Mus musculus"
/cell_line="normal T-cell line L12"
/cell_type="Ab-MuLV transformed Meth A fibroblast"
/cequanced_mol="cDNA to mRNA"
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                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                    Zakut-Houri,R., Oren,M., Bienz,B., A single gene and a pseudogene for Nature 306 (5943), 594-597 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Analysis of the gene coding for the p53
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Similarity 100.0%;
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/taanslation="MTAMEESQSDISLELPLSQETESGLMKILEPEDILESPHCMDDLLLPQDVEEFEGES EALRYSGAPAAQDPVTETPGPVAPAPATPWPLSSTVPSQKTYQG
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KKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE
PPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTITTLEDSSGNLLGRDSFEKRVCACPG
                                                                                                                                                                                             /usedin=X00876:P53_mRNA
25 c 35 g
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                                                                                                                                                                                                                             /usedin=X00876:P53_CDS
                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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Pred. No. 8.05e-03;
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Pred. No. 1.43e-03;
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the cellular
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MUSP53B

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02-NOV-1992

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US-08-644-289-4.rgc

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DEFINITION

REFERENCE AUTHORS COMMENT SOURCE **LOCUS** မှ Db FEATURES ACCESSION DEFINITION ORIGIN BASE COUNT FEATURES **EYWORDS** TITLE Matches MEDLINE JOURNAL ORGANISM Query Match 70.0%; Best Local Similarity 100.0%; 1183 agacagcagggctcactccag 1203 CDS source source 8 AGACAGCAGGCTCACTCCAG 10 g53570 X00741 MMP53 Data kindly reviewed (19-FEB-1986) by A. Wade-Evans Cloning and expression analysis of full length mouse Mus musculus Nucleic Acids Res. 12 (14), 5609-5626 (1984) encoding the transformation associated protein p53 Jenkins, J.R., Rudge, K., Redmond, S. and Wade-Evans, A. Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Cho: oncogene. Mouse mRNA 84272240 Sciurognathi; Myomorpha; Muridae; Murinae; Mus. Tetrapoda; Amniota; Mammalia; Theria; Eutheria; house mouse. 21; (bases 1 to 1377) 299 Conservative മ KKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE
PPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPG
RDRRTEEENFRKKEVLCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTLKIRGRKR NYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIY KSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYEP /organism="Mus musculus" 123..1292 Location/Qualifiers
1..1377 FEMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD\* LLPQDVEEFFEGPSEALRVSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQKTYQG /db\_xref="PID:g200199" /translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL /sub\_species="domesticus" /cell\_type="nontransformed helper T-cell" EMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD" DRRTEEENFRKKEV LCPELP PGSAKRALP TCTSASP PQKKKP LDGEYFTLK I RGRKRF PEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGR YGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYK LLPRDVEEFFEGPSEALRVSGAPAAQDPVTETPGQWPAPATPWPLSSFVPSQKTYQGN translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL/ /db\_xref="PID:g53571" /note="p53" /codon start=1 /sequenced\_mol="cDNA to mRNA" /strain="BALB/ /codon\_start=1 /product="p53 protein" 113..1285 /organism="Mus musculus" Location/Qualifiers for transformation associated protein p53. 1377 bp 385 c Score 21; DB 67; Pred. No. 8.05e-03; <u>.</u> 334 g Mismatches 267 t 0 Length 1285; Indels Glires; Rodentia; 0; 12-SEP-1993 cDNA sequences Gaps Chordata; <u>.</u>.

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Mar 25 02:

exon	CDS	exon	exon misc_signal	REFERENCE 1 (base AUTHORS Weghorst TITLE Cloning JOURNAL Gene 166 MEDLINE 96125211 COMMENT NCBI gi: FEATURES	RESULT 7 LOCUS RATPSEUDO DEFINITION RATTUS no ACCESSION L12046 NID 9206472 KEYWORDS tumor sup SOURCE Rattus no ORGANISM Rattus no Eukaryota Vertebrat	BASE COUNT 3 ORIGIN Query Match Best Local Simi Matches 21; Db 1190 agacago:                     Cp 30 ACACACC
/codon_start=1 /codon_start=1 /db_xref="PID:g206473" /translation="KVQRKPSKQLLPHRNLELRPISILKNLSQLWLSSGLPAVSDNQ /translation="KVQRKPSKQLLPHRNLELRPISILKNLSQLWLSSGLPAVSDNQ VCYVHYVLPSPKLAILPAGEDMPCAVMGQLHTSNWHLCACHGIYKKSQHWTEVMRRCSH HERCSDGDDQTPPPYPTSILSG" 316498 /gene="p53 PG-III" /note="this region of the pseudogene corresponds to exon 5 of the rat p53 cDNA; putative" 499746 /note="this region of the pseudogene corresponds to exon 6	/note="his region of the pseudogene corresponds to exon 4 of the rat p53 cDNA; putative" <168>542 /gene="p53 PG-III" /gene="p53 PG-III" /gene="rumor suppressor; this region of the pseudogene is a potential open reading frame; putative; NCBI gi: 206473"	region of the pseudogene corresponds to exon p53 cDNA; putative p55 cDNA; putative p55 cDNA; putative p55 cDNA; p55 cD	orresponds to e	Rais 1, C.1 and and 1 s (2) Lo	# U 5 5 F 5 C	316 a 422 c. 348 g 291 t  tch 70.0%; Score 21; DB 64; Length 1377;  al Similarity 100.0%; Pred. No. 8.05e-03; 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  agacagcaggagtcactccag 1210

DEFINITION ACCESSION BASE COUNT ORIGIN REFERENCE SOURCE NID RESULT ဌ Mar 25 02-50 FEATURES KEYWORDS TITLE 70.0%;
Best Local Similarity 100.0%;
Matches 21; Conservation ORGANISM JOURNAL AUTHORS 1011 agacagcagggctcactccag 1031 exon exon exon exon exon exon exon CDS source misc\_signal misc\_signal 30 AGACAGCAGGGCTCACTCCAG 10 RATPSEUDO 1447 bp DNA ROD 07-JUN-1993 Rattus norvegicus p53 tumor suppressor pseudogene, partial ORF. L12046 Rattus norvegicus (strain Fisher 344) male liver DNA. Rattus norvegicus  $\,$ Unpublished (1993) Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

1 (bases 1 to 1447) Weghorst, C.M., Buzard, G.S., Hulla, J.E., Calvert, R.J. and Rice, J.M. tumor suppressor. g206472 Nucleotide sequence of a rat p53 pseudogene: a representative the family of p53 pseudogenes in the rat genome 366 /note="this region of the pseudogene corresponds to exon 3 of the rat p53 cDNA; putative"

98..315 /note="this region of the pseudogene corresponds to exon 4 of the rat p53 cDNA; putative" <168...>542/note="this region of the pseudogene corresponds to exon 2
of the rat p53 cDNA; putative" 1..1447 /note="this region of the pseudogene corresponds to exon 10 of the rat p53 cDNA; putative" 1107..1109 /note="this site within the pseudogene corresponds to the translation stop site of the rat p53 cDNA; putative" a 388 c 336 g 357 t /note="this region of the pseudogene corresponds to of the rat p53 cDNA; putative" 883..937 /note="this site within the pseudogene corresponds to the ATG translation start site of the rat p53 cDNA; putative" /tissue\_type="liver"
1..75 /note="this region of the pseudogene corresponds to exon 9
of the rat p53 cDNA; putative" /note="this region of the pseudogene of the rat p53 cDNA; putative" of the rat p53 cDNA; putative 747..882 /sequenced\_mol="DNA" /sex="male" /strain="Fisher 344" /organism="Rattus norvegicus" Location/Qualifiers 1032..1447 938..1031 Score 21; DB 91; Length 1447; Pred. No. 8.05e-03; 0; US-08-644-289-4.rgc Mismatches 0; Indels 0; corresponds to Gaps exon 8 exon 0;

/note="this region of the pseudogene is a potential open

US-08-644-289-4.rgc

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Best Local Similarity 100.0%;
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L12046;
16-MAR-1993 (Rel. 35, Created)
14-APR-1996 (Rel. 47, Last updated, Version 3)
Rattus norvegicus p53 (PG-III) pseudogene, partial
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                                                                                                                                                       Weghorst C.M., Buzard G.S., Calvert R.J., Hulla J.E., Rice J.M.; "Cloning and sequence of a processed p53 pseudogene from rat: a potential source of false 'mutations' in PCR fragments of tumor DNA";
                                                                                                                                                                                                                                                      Rattus norvegicus (rat)
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Eukaryota; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
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/note="this site within the pseudogene corresponds to the translation stop site of the rat p53 cDNA; putative" a 388 c 336 g 357 t
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VCYVHVLPSPKLAILPAGEDMPCAVMGQLHTSNWHLCACHGIYKKSQHWTEVMRRCSH
/tissue_type="liver"
                                    /organism="Rattus norvegicus"
/strain="Fischer 344"
                                                                                                      Location/Qualifiers
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                    /sex="male"
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RESULT LOCUS DEFINITI ACCESSIC NID KEYWORDS	Ср	Qu Be Ma	S F F F F	FT T	FIFT	F17	F F F	**************************************	FI FI	v 	, F. F.	7 7 F 7	F F F	# # # # # #	F F F F
RESULT 10 LOCUS DEFINITION ACCESSION NID KEYWORDS	1011 a     30 A	Query Match Best Local Matches	misc_sig	exon	exon	exon	exon	exon exon			. (		exon Son	exon	exon misc s
RNP53 Rat mRNA fo X13058 g56828 oncoprotein	gacagcag          SACAGCAG		nal 1447												xon isc_signal
- H	agacagcagggctcactccag 	70.0%; Similarity 100.0%; 21; Conservative	of the rat 11071109 /note="this translation BP; 366 A; 38	/note= this of the rat p 10321447 /note="this	/note="this of the rat 9381031	/note="this of the rat 883937	/note="this of the rat 747882	316498 /gene="p53 /note="this of the rat 499746	CYVHVI	potential /codon_st /db_xref= /translat	/gene="p53 /note="tum	/note="this of the rat	/note=" of the 98.315	/note="this ATG transla 7697	175 /note=" of the 24
27 bp clear	ccag 1031			rat p53 1447 "this rec	hi at	hi at	hi at	98 "p53 PG "this re rat p5:	PSPKLAII DQTPPPYI	ial open start=1 ef="PID: lation="	e e	thi rat	thi rat	"this	"this re rat p53
RNA oncoprotein	31	Score 21; Pred. No. 0; Misma	cDNA; ce with op site ; 336 (	cDNA;	gion o cDNA;	s region of p53 cDNA; p	s region of p53 cDNA; p	PG-III" s region of p53 cDNA;	CYVHYLPSPKLAILPAGEDMPCAVMGQLHTSNWHLCACHGIYKKSQHMTEVMRRCSHH RCSDGDDQTPPPYPTPSILSG"	potential open reading frame; putative; NCBI gi: 206473" /codon_start=1 /db_xref="PID:g206473" /translation="KVQRKPSKCQLLPHRNLELRPLSLLKNLSQLWLSSGLPAVSDNQ	PG-III"	s region of p53 cDNA; p	s region of p53 cDNA; p	site with tion start	gion o cDNA;
in p53.		21; DB 12; No. 8.05e-03 Mismatches	utativ n the of the 357 T	putative' f the pseu	f the pseu putative	the pseudogene putative"	f the pseu putative	f the pseudogene putative"	CAVMGQLHI	y frame; ' 'CQLLPHRU	or; this	the pseudogene putative"	the	within the postart site of	f the pseu putative"
ROD		Length 14 3; 0; Indels	e" pseudogene cori rat p53 cDNA; ; 0 other;	pseudogene o			pseudogene (	idogene c	rsnwhlca	putative; NLELRPLSLL	region		pseudogene d	e pseudogene of the rat p	pseudogene ( ive"
12-s:		1447; els 0;	corr DNA;	corresponds	correspo	corresponds	corresponds	corresponds	CHGIYKKSI	e; NCBI	of the p	corresponds	corresponds	e corresponds p53 cDNA; pu	corresponds
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SOURCE

Norway rat.

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Best Local Similarity 100.0%;
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                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1097 agacagcagggctcactccag 1117
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                                            Zakut-Houri, R., Oren, M., Bienz, B., Lavie, V., Hazum, S. and Givol, D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306, 594-597 (1983)
                                                                                                                                                                                                              Mouse embryo F9 carcinoma cells, cDNA to mRNA, p422, p208 [1], and clone pp53-1 [2].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of a cDNA encoding the rat p53 nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                               DNA-binding protein; antigen; p53 gene; tumor antigen.
                                                                                                                                                                                                                                                                                           g200204
                                                                                                                                                                                                                                                                                                                       K01700
                                                                                                                                                                                                                                                                                                                                         Mouse p53 cellular tumor antigen, mRNA.
                                                                                                                                                                                                                                                                                                                                                                     MUSP53M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Data kindly reviewed (09-Feb-1989) by Soussi T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 16 (23), 11384 (1988)
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Moleculaire, IRSC - CNRS, BP 08 94802 Villejuif, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-SEP-1988) to the EMBL/GenBank/DDBJ databases.
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                       84068204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
                                                                                                                                                                    Eukaryota; Animalia; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 1627)
(bases 105 to 1772)
                                                                                                               cheria; Rodentia; Myomorpha; (bases 1 to 1716)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPPEVGSDYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MEDSQSDMSIELPLSQETFSCLWKLLPPDDILPTTATGSPNSME
DLFLPQDVAELLEGPEEALQVSAPAAQEPGTEAPAPVAPASATPWPLSSSVPSQKTYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell
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                                                                                                                                                                                                                                                                                                                                                                 1772 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 69;
Pred. No. 8.05e-03;
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                                                                                                                                                                                                                                                                                                                                                                     DRNA
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                                                                                                                                             Muridae; Murinae.
                                                                                                                                                                    Vertebrata; Mammalia; Theria;
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COMMENT
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sequence of the murine p53 psuedogene, also reported by [1] (see separate entry), and the cDNA sequence are almost identical from nucleotide 186 onward. Upstream of this position the two sequences
                                                                                                                           There is only one functional p53 gene in the mouse genome. All existing different forms of murine p53 must be products of the same gene, mostly due to post-translational modifications [1]. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The murine p53 protein is similar to the avian and human myc gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The amino acid sequence of murine p53 determined from a cDNA clone Virology 134, 477-482 (1984)
                                                                                                                                                                                                                                                             sequence of cDNA in [1] was established by analysing four separate cDNA clones; p176 (bp 1-1247), p271 (bp 69-638), p422 (bp 1288-1719), and p208 (bp 1432-1719) [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                    are localized in the nucleus of tranformed cells. The Ela proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennica, D., Goeddel, D.V., Hayflick, J.S., Reich, N.C., Anderson, C.W.
                                                                                                                                                                                                                                                                                                                                                                                            and p53 have been shown to have very short half-lives [2]. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins are rich in proline, contain proline runs or clusters, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           products and the adenovirus Ela proteins. All three of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86072076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Levine, A.J
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
165 bp upstream of NcoI site.
                                                                                                                                                                                                                                                                                                                                                                                          /gene="p53"
/map="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="carcinoma"
<1..1668</pre>
                                                   FEMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD*
                                                                                                                                                                                                    /product="cellular tumor antigen"
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                                                                                                    PPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPG
                                                                                                                             KKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE
                                                                                                                                                        LLPQDVEEFFEGPSEALRVSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQKTYQG
NYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIY
                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequenced_mol="cDNA to mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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                           546 c
                           412 g
                           429 t
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FEATURES

relative to the cDNA [1].

substitutions and to some small deletions or additions in this gene the two sequences differ by only 4%. The differences are due to deverge totally and no homology can be observed; downstream of here

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FOCUS.
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                        DEFINITION
                                                                                                                                                                                       ORIGIN
             ACCESSION
                                                                                                                                                   Best
                                                                                                                                                             Query Match
                                                                                                  1228 agacagcagggctcactccag 1248
                                                                                                                             70.0%;
t Local Similarity 100.0%;
ches 21; Conservation
                                                                                      30 AGACAGCAGGGCTCACTCCAG 10
g53575
           Mouse mRNA for cellular X01237 K01700
                                     MMP53R
                                   1773 bp
                                                                                                                                                Score 21; DB 67;
Pred. No. 8.05e-03;
                                                                                                                                      0;
                       tumour antigen p53
                                                                                                                                      Mismatches
                                                                                                                                      <u>.</u>
                                                                                                                                                            Length 1772;
                                                                                                                                      Indels 0;
                                     12-SEP-1993
                                                                                                                                    Gaps
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EYWORDS

antigen; tumor antigen.

Mar 25 02:50

US-08-644 289-4.rge

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Analysis of the gene coding for the murine cellular tumour antigen {\mathfrak p}53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-NOV-1985) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Givol, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bienz, B., Zakut-Houri, R., Givol, D. and Oren, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
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                                                                                                                                                                                                                                          /citation=[1]
859
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561
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404
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158..1330
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1558..1559
                                                           /citation=[1]
1503
                                                                                                                                                                                                                                                                             /note="A is G
                                                                                                                                                                                                                                                                                                                    /citation=[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLP QDVEEFFEGP SEALRVSGAP AAQDP VTETP GP VAP AP AT PWP LSSF VP SQKT YQ G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="p53 polypeptide (aa 1-390)"
                                        /note="U is A in [1]"
                                                                                                /note="CU is UC
                                                                                                                     1447..1448
                                                                                                                                       /citation=[1]
                                                                                                                                                          /note="UA is CU
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REFERENCE
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                                                                                                                                     70.0%;
al Similarity 100.0%;
21; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol,D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306, 594-597 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse p53 cellular tumour antigen psuedogene.
 MMP53P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse 3.3-kb fragment isolated from a BALB/c genomic library, clone
                                                                                                                                                                                                                                                                                                                                                                                                                        the two sequences differ by only 4%. The differences are due to substitutions and to some small deletions or additions in this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide 186 onward. Upstream of this position the two sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             separate entry), and the psuedogene are almost identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The DNA sequence of pCh53-11 contains a long poly-A tract, lacks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84068204
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Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          relative to the cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         deverge totally and no homology can be observed; downstream of here
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of the murine p53 cDNA, also reported by [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from reverse transcription of the mature mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1852-1864), suggesting that it is a processed gene which resulted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 introns, and is bounded by direct repeats (bp 169-181 and bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pCh53-11.
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Indels

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Rodentia;

0511, National University of Singapore, Lower Kent Ridge Singapore Road, Singapore

BASE COUNT ORIGIN FEATURES Best Matches exon CDS exon source Local ch 66.7%; 1 Similarity 88.5%; 23; Conservative 328 ۵ gene" /pseudo 888..961 /pseudo 359..539 /pseudo 24..1245 /pseudo 15..97 /clone="pR53P1" /strain="Wistar" /pseudo gene\* /note="corresponds /gene="p53" /note="corresponds /pseudo 751..887 641..750 540..640 98..119 /note="corresponds to a /tissue\_type="liver" /cell\_type="hepatocyte" 962..1153 /note="corresponds /note="corresponds /gene="p53" /note="corresponds /gene="p53" /note="corresponds /gene="p53" /note="corresponds /sex="male" organism="Rattus norvegicus" 154..>1273 'pseudo 'pseudo note="corresponds gene="p53" /gene="p53" 'pseudo note="corresponds /gene="p53" pseudo 20..358 'pseudo 'note="corresponds to exon 3 of the rat p53 gene" /gene="p53" pseudo /gene="p53" ocation/Qualifiers 356 c Score 20; DB 70; I Pred. No. 4.36e-02; 0; Mismatches 3; 306 g to a ç ç ţ ç ç ţ to exon ç exon exon exon exon exon exon exon 283 part of part of 4 of 6 S 10 9 of. ef. of. of ٥f ef. of. 3 Length 1273; exon the the the the the rat the rat the rat p53 exon 1 of the rat p53 the Indels rat rat rat rat 1 rat **p**53 **p**53 **p**53 **p**53 **p**53 **p**53 of the rat p53 p53 ٥, gene" gene" gene" gene" gene" gene" Gaps 9

맑 1039 agacagcagggctcactcctgcctcc 1064

Department of Microbiology,

processed p53 pseudogenes from

Myomorpha;

CP 30 AGACAGCAGGCTCACTCCAGGATCC 5

Search completed: Tue Mar 25 02:52:18 1997 Job time :  $63\ secs$ .

\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* ----Œ

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intellicenetics, Inc.

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:53:15 1997; MasPar time 56.30 Seconds 234.987 Million cell updates/sec

Tabular output not generated.

Perfect Score: Description: Title: (1-30) from US08644289.seq >US-08-644-289-4

N.A. Sequence: Comp: 1 AGTCGGATCCTGGAGTGAGCCCTGCTGTCT 30 TCAGCCTAGGACCTCACTCGGGACGACAGA

Scoring table: TABLE default

Gap 10

Nmatch STD: Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST27 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 26:EST26 27:EST27 26:EST26 27:EST27 26:EST26 27:EST27 28:EST28 20:EST30 31:EST31 32:EST33 33:EST33 34:EST34 35:EST35 36:EST36 31:EST31 32:EST38 33:EST37 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38 39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44 45:EST45 56:EST56 57:EST57 58:EST55 55:EST55 54:EST56 67:EST56 57:EST57 58:EST55 59:EST59 60:EST66 67:EST61 62:EST66 63:EST66 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68 69:EST69 70:EST70 77:EST77 72:EST72 73:EST73 74:EST74 75:EST75 76:EST76 83:EST88 89:EST88 384:EST88 79:EST98 86:EST86 87:EST98 90:EST99 91:EST99 92:EST99 93:EST99 94:EST98 95:EST96 97:EST97 98:EST98 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 :EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8

Database:

EST-STS-TWO

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100:EST100 101:EST101 102:EST102 103:EST103 104:EST104 105:EST105 106:EST106 107:EST107 108:EST108 109:EST109 110:EST110 111:EST111 112:EST112 113:EST113 114:EST114 115:EST115 116:EST116 117:EST117 118:EST118 119:EST119 120:EST120 121:EST121 122:EST122 123:EST123 124:EST124 125:EST125 126:EST126 127:EST127 128:EST128 129:STS1

Mar 25 02:52

### US-08-644-289-4.rst

173:enSTS1 174:enSTS2 130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7 136:STS8 137:STS9 138:STS10 139:weEST 140:gnEST1 141:gnEST3 142:gnEST3 143:gnEST3 143:gnEST3 144:gnEST5 145:gnEST6 146:gnEST3 147:gnEST3 148:gnEST9 149:gnEST10 150:gnEST11 151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST15 159:gnEST3 155:gnEST14 154:gnEST2 159:enEST3 150:enEST4 154:gnEST3 150:enEST4 154:gnEST5 159:enEST3 150:enEST4 154:gnEST5 159:enEST3 159:gnEST4 154:gnEST5 159:enEST3 159:gnEST4 154:gnEST5 159:enEST3 159:gnEST4 154:enEST8 159:gnEST4 154:enEST5 159:gnEST4 154:enEST8 159:gnEST4 154:enEST5 159:gnEST4 154:enEST8 159:gnEST4 154:enEST8 159:gnEST4 159:gnEST5 159:gnEST4 159:gnEST5 165:enEST9 166:enEST10 167:enEST11 168:enEST12 169:enEST13 170:enEST14 171:enEST15 172:enEST16

Statistics: Mean 7.041; Variance 1.665; scale 4.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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N70695 N34722 H23094

1.13e+00

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US-08-644-289-4.rst

RESULT LOCUS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens DNA. tetranucleotide repeat.

REFERENCE

(bases 1 to 269)

AUTHORS

Melis,R.,

KEYWORDS ACCESSION DEFINITION

L30902

Human STS UT5411, HUMUT5411B

269

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g604971

0,

LOCUS

HUM030E06B

303 bp

mRNA

26-AUG-1995

0; Gaps

9

ACCESSION DEFINITION RESULT

g960530

Human fetal brain cDNA 5'-end GEN-030E06. D59424

KEYWORDS

EST(expressed sequence tag); Human fetal brain; similar to none(May 29,1995).

Homo sapiens (library: Clontech human fetal brain polyA+ mRNA

ORGANISM

Homo sapiens

(#6535)) cDNA to mRNA.

sequence tagged sites from the human genome Unpublished (1994) See COMMENT for author address Gel: Acrylamide 7%, Formamide 32%, Urea 34% microsatellite marker; sequence tagged site; PCR primer; STS sequence; microsatellite DNA; Primer A: CAGCCACATGCTCACTTTGGGAAC e-mail: sts@corona.med.utah.edu Utah, Dept. of Human Genetics 2160 Eccles Institute of Human Genetics Submitted by: Utah Center for Human Genome Research University of Genetic and physical mapping of simple sequence repeat containing Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Initial Denaturation: 94C 300sec Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and Denaturation A c. 74 C 10 sec. 10 sec. 72 C 20 s Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., CATTCCACCCCCTCACAGCTTAGA ALI GNMENTS primer bind Annealing Extension ec. 72 C 20 sec. 30 20 sec. Mg++: 1.00 mM za32d02.sl Homo sapie yx82b12.rl Homo sapie ym51d09.s1 Homo sapie STS 28-DEC-1994 30 94 C 1.13e+00 1.13e+00 10 sec. မှ Вb COMMENT ORIGIN BASE COUNT FEATURES REFERENCE SOURCE KEYWORDS Matches Query Match 56.7%; Best Local Similarity 83.3%; AUTHORS ORGANISM JOURNAL source 262 acagaagggctcactccncaatcc 285 28 ACAGCAGGCTCACTCCAGGATCC 5 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Unpublished (1995) Eucaryotae; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 295) Homo sapiens Source: IMAGE Consortium, LLNL Contact: Wilson RK WashU-Merck EST Project GDB: G00-399-901 Wilson, R. normalization. Library constructed by Bento Soares and M.Fatima the Lafmid BA vector. Library went through one round of Not I and directionally cloned into the Not I and Hind III sites of human clone=27554 library=Soares infant brain lNIB vector=Lafmid BA g766048 High quality sequence stops: 233 Email: est@watson.wustl.edu Fax: 314 286 1810 The WashU-Merck EST Project Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Bonaldo. 20; This clone is available royalty-free through LLNL ; contact the MAGE Consortium (info@image.llnl.gov) for further information. 314 286 1800 78 Conservative മ /note="human" a 72 c /organism="Homo sapiens" /clone="27554" Location/Qualifiers Score 17; DB 75; Pred. No. 8.05e-03; 0; Mismatches 59 g 85 4 4 Length 295; Louis, 1 others Indels Gnathostomata; Mammalia;

MO 63108

COMMENT

Cycles

74 C 10 sec.

10 sec.

End to Label: Primer B

PCR Profile:

Primer B:

Salt Lake City, UT 84112

JOURNAL

TITLE

White, R.

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Best Local Similarity 62.1%;
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                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 AGACAGCAGGGCTCACTCCAGGATCCGAC 2
                                                                                                                                                                                               Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                   EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zein.
Unpublished (1994)
                                                                                 Shen, B., Carneiro, N., Torres-Jerez, I., Helentjaris, T., Habben, J., Larkins, B.,
                                                                                                                                                                                                                                                                                 strand to RNase-nicked DNA:RNA hybrid with DNA Poll. Sall adaptors were added to the ends, the ds-cDNAs were then digested with NotI
                                                                                                                                                                                                                                                                                                                       strain=W64A2 vector=ZipLox host=DH10B primer=T3 Rsite1=SalI Rsite2=NotI ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT oligomer and then adding the second
                                                                                                                                                                                                                                                                                                                                                                                                                                        g485661
                                                                                                                                                                                                                                                                                                                                                                                                                                                              T18731
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463-10 kagasuno Kawauchi-cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Otsuka GEN Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catarrhini;
                                          Single-Pass Sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                       Eucaryotae; Embryophyta; Magnoliophyta; Liliopsida; Cyperales;
                                                                                                                                                                                                                                      phage vector, excised as plasmids,
                                                                                                                                                                                                                                                            and size-selected. These were directionally-cloned into the ZipLox
                                                                                                                                                                                                                                                                                                                                                                                         maize clone=2C01B05 library=membrane-free polysomes from endosperm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsutomu Fujiwara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-May-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maekawa, H., Shin, S. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E.-I., Hirai, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                               Baysdorfer,C
                                                                                                                                                    Poaceae; Zea.
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Pred. No. 8.05e-03;
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                                                                               Almira, E., Ferl, R. and
                                                                                                       Stevenson, R.,
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Best Local Similarity 90.5%;
source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthy Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                           Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                   Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human clone=159293 library=Soares breast 3NbHBst vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H14461
                                                                                    Source: IMAGE Consortium, LLNL
                                                                                                         High quality sequence stops: 310
                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                       Fax: 314 286 1810
                                                                                                                                                                                                 4444 Forest Park Parkway,
                                                                                                                                                                                                                      Washington University School of Medicine
                                                                                                                                                                                                                                                                                                             Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                           Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of normalization to a Cot = 20. Library constructed by Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified pT7T3 vector (Pharmacia). Library went through one round
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 digested with Not I and cloned into the Not I and Eco RI sites of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact:
                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                            Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 448)
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Best Local Similarity 83.3%;
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Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.—J., Dinke, D., Feng, P., Ferrie, A.,
Coleman, T.A., Collins, E.—J., Dinke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.—W., Hu, J.—S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.—F., Wing, J., Xu, C.,
Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
                                                                                                                                                                                                                                                                                                     Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., EitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                          Other_ESTs: THC11831
                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
                                                                                                                                                                            For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human primer=M13 Reverse library=Human Embryo.
                                                                                                                                                                                                                                                              Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                             Based Upon 52 Million Basepairs of cDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial Assessment of Human Gene Diversity and Expression Patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
                                                                                                                                                      (tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                               £mail: tdbinfo@tdb.tigr.org
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                                                  /organism="Homo sapiens"
/note="human"
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/clone="159293"
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Pred. No. 8.05e-03;
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                                                                                                                                                      174 gtcggatcctggagtccatccagctg 199
                                                                                                                                                                                                                      Local
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                                                                                                                                     2 GTCGGATCCTGGAGTGAGCCCTGCTG 27
            za89b07.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 299701 5' similar to gb:L19067 TRANSCRIPTION FACTOR P65 (HUMAN);.
                                                                                                                                                                                                   ch 53.3%;
1 Similarity 80.8%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
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EST(expressed sequence tag).
Caenorhabditis elegans (strain N2, ) (library: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toward an expression map of the C.elegans genome Unpublished (1995)
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g1278511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-Aug-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishigaki, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unpublished cDNA) Hermaphrodite embryo embryo cDNA to
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Similarity 90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email:ykohara@ddbj.nig.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phone: 0559-81-6854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yata 1111, Mishima Shizuoka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene Library Lab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yuji Kohara
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                                                                                                                                                                                                                                                                                                                          /tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                          /sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                            sequenced_mol="cDNA to mRNA"
                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="embryo"
                                                                                                                                                                                                                                                                                                                                                                                              /strain="N2"
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Pred. No. 1.00e-01;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
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Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   !MAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ⊡mail: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 314 286 1810
                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 305)
                                             standard; RNA;
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                                                                                                                                                                                                                                                                                                                                                       <1..>305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Not I and Eco RI sites of a modified pT7T3 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was size selected, ligated to Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares fetal lung NbHL19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="299701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetal heart NbHH19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adapters (Pharmacia), digested with Not I and cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from the same fetus as the fetal heart library, Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                         53.3%;
79.2%;
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                                             EST;
                                                                                                                                                                                                                                         Score 16; DB 147;
Pred. No. 1.00e-01
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                                                                                                                                                                                                                                                              Length 305;
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                    ORGANISM
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for
                                                                                                                                                                                                                                                                                                                                                            Sequence 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: mob.REGA+ET High quality sequence stop: 1. NCBI gi: 1278511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further information. Trace considered overall poor quality Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The WashU-Merck EST Project";
                                                                                                                                                                                                                                   184 ggatcctgnagagagcagtgcngt 207
                                                                                                                                                                                                                                                                                                      y Match 53.3%;
Local Similarity 79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to gb:L19067 TRANSCRIPTION FACTOR P65
                                                                                                                                                                                                                  5 GGATCCTGGAGTGAGCCCTGCTGT
                                                                                                                                                              10
                                                                                                         C.elegans cDNA clone yk90h9 : 3' D72177
                    Caenorhabditis elegans
                                 Caenorhabditis elegans (strain N2, ) (library: Yuji Kohara unpublished cDNA) Hermaphrodite embryo embryo cDNA to mRNA
                                                                      EST (expressed sequence tag).
                                                                                       g1111884
Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
                                                                                                                                              CELK090H9R
                                                                                                                                                                                                                                                                                       19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 47, Last updated, Version 1)
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                            В₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into
                                                                                                                                                                                                                                                                                                                                                       81 A; 66 C; 82 G; 66 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soares and M.Fatima Bonaldo. This library was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      normalization to a Cot = 5. Library constructed by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Not I and Eco RI sites of a modified pT7T3 vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the same fetus as the fetal heart library,
                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares fetal lung NbHL19W"
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                                                                                                                                                                                                                                                                                                        Pred. No. 1.00e-01;
                                                                                                                                                                                                                                                                                                                       Score 16; DB 164;
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RESULT 11
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Best Local Similarity 80.8%;
                                                                                                                                                                                                                  AUTHORS
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                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H32097
                                                                                                                                                                      Fuldner,R.A., Marmaras,S., Glodek,A., Gocayne,J.D., Adams,M.D.,
Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                     Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                   rat primer=M13 Reverse library=Rat PC-12 cells, untreated vector=pBluescript SK- Rsite1=EcoRI Rsite2=XhoI poly(A)+ RNA was purified from untreated PC12 cells cultured for 9 days. cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g977514
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Kohara, Y., Motohashi, T., Tabara, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Caenorhabditis.
                                             Contact: Lee NH
                                                                                                                             expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                  Comparative expressed sequence tag analysis of differential gene
                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha;
                                                                                                                                                                                                                                                                                                                                       constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP\ II\ Vector\ Kit\ by\ Stratagene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email:ykohara@ddbj.nig.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
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                                                                                                           tactor treatment
                                                                                                                                                                                                            Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A.
                                                                                                                                                                                                                                                        Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                  (bases 1 to 320)
Institute for Genomic Research Clopper Rd, Gaithersburg, MD 2
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/clone_lib="Yuji Kohara unpublished cDNA"
1 57 c 80 g 88 t
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 Query Match 53.3%;
Best Local Similarity 80.8%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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Best Local Similarity 94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: nhlee@tigr.org
For clone availability please contact
(tdbinfo@tdb.tigr.org).
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-Aug-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                         Toward an expression map of the C.elegans genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unpublished cDNA) Hermaphrodite embryo embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST (expressed sequence tag).
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                                                                                                                                                                                                                                                                       Fax : 0559-81-6855
                                                                                                                                                                                                                                                                                          Phone: 0559-81-6854
                                                                                                                                                                                                                                                                                                                                       National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                          Yuji Kohara
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                                                                                                                                                                                                                                                                                                         111 Japan
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                                                                                                                                                                                                                                                                                                                                                        Gene Library Lab.
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                                                                                 /sequenced_mol="cDNA to mRNA"
/sex="Hermaphrodite"
/tissue_type="embryo"
/clone_lib="Yuji Kohara unpublished cDNA"
/clone_lib="Yuji Kohara unpublished cDNA"
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Best Local Similarity 94.4%;
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 163
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Fax: 314 286 1810
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/clone="129011"
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TOCUS Ş 밁 KEYWORDS ACCESSION ORIGIN DEFINITION RESULT BASE COUNT FEATURES REFERENCE SOURCE KEYWORDS REFERENCE SOURCE ACCESSION TITLE AUTHORS ORGANISM Matches Query Match 53.3%; Best Local Similarity 80.8%; AUTHORS ORGANISM JOURNAL source 15 CELKIllCZR 334 bp mRNA EST 10 C.elegans cDNA clone ykll1cl2 : 3' end, single read. Caenorhabditis elegans Caenorhabditis elegans (strain N2, ) (library: Yuji Kohara unpublished cDNA) Hermaphrodite embryo embryo cDNA to mRNA g1112628 D72916 D72892 Submitted (23-Aug-1995) to DDBJ by: Unpublished Toward an expression map of the C.elegans genome Nishigaki, A. Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and Rhabditidae; Caenorhabditis. Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; EST (expressed sequence tag). 411 Japan Gene Library Lab. National Institute of Genetics Yata 1111, Mishima Shizuoka Submitted (23-Aug-1995) to DDBJ by: Unpublished (1995) Toward an expression map of the C.elegans genome Nishigaki, A. Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Caenorhabditis elegans unpublished cDNA) Hermaphrodite embryo embryo cDNA to mRNA Caenorhabditis elegans (strain N2, ) (library: Yuji Kohara EST (expressed sequence tag). Yuji Kohara Email:ykohara@ddbj.nig.ac.jp Phone: 0559-81-6854 Yuji Kohara Rhabditidae; Caenorhabditis. g1112607 21; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; (bases 1 to 334) (bases 1 to 329) 95 : 0559-81-6855 Conservative ø /sex="Hermaphrodite"
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exon 10.			Bacillus subtilis DNA 8.12e+02	fr 8.	Human DNA sequence fr 8.12e+02		00 0	Caenorhabditis elegan 8.12e+02		Haemophilus influenza 8.12e+UZ Caenorhabditis elegan 8.12e+UZ		Pseudomonas fluoresce 8.12e+02 Haemonhilus influenza 8.12e+02		S.cerevisiae chromoso 8.12e+02 S.cerevisiae chromoso 8.12e+02	Drosophila persimilis 8.12e+02		Drosophila pseudoobsc 8.12e+02	pseudoobsc 8.1	Drosophila pseudoobsc 8.12e+02		pseudoobsc 8.	Drosophila pseudoobsc 8.12e+02	pseudoobsc	Drosophila pseudoobsc 8.12e+02	pseudoobsc 8.	Drosophila pseudoobsc 8.12e+02		Drosophila pseudoobsc 8.12e+02		_		Unidentified marine e 8.12e+02	E.granulosus EgHbx2 h 8.12e+02	. !	Description Pred, No.	SUMMARIES

Statistics:

Mean 5.503; Variance 1.579; scale 3.486

RESULT 1

IOCUS MUSCCC210 1.53 bp DNA ROD
DEFINITION Mouse complement component C2 gene, exon 10.
ACCESSION M60572 J05661

NID g192424

KEYWORDS complement component C2.
SEGMENT 10 of 18
SOURCE Mouse DNA.
ORGANISM Mus musculus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Submitted (12-JUN-1992) G.C. Oliver, Max-Planck-Inst of Biophysical Chemistry, Dept of Cell Biology, Am Fassberg 3400, Goettingen, FRG
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                                                                                                          Submitted (18-APR-1996) Vispo M., Dpto. Genetica. Facultad Biologia, Av. Diagonal 645, 08071 Barcelona, Spain E-mail:
                                                                                                                                                                                                  Gene 121 (2), 337-342 (1992)
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                                                                                         vispo@porthos.bio.ub.es
                                                                                                                                                Direct Submission
                                                                                                                                                                 Vispo, M.
                                                                                                                                                                                                                                    Homeoboxes in flatworms
                                                                                                                                                                                                                                                                                                              Revised by [3]
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order(M60571:97..102,1..6)
/organism="Echinococcus granulosus"
1..141
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Pred. No. 8.12e+02;
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BASE COUNT ORIGIN f မှ В BASE COUNT **LOCUS** B ORIGIN FEATURES COMMENT REFERENCE REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION RESULT TITLE Matches TITLE ORGANISM Matches Query Match 100.0%; Best Local Similarity 100.0%; Query Match 100.0%; Best Local Similarity 100.0%; JOURNAL JOURNAL AUTHORS AUTHORS rRNA exon source intron 338 aggcatgcct 347 730 aggcatgcct 739 10 AGGCATGCCT 1 10 AGGCATGCCT 1 MEU41091 956 bp DNA BCT 02-MAY-1996 Unidentified marine eubacterium Hstpl6 16S ribosomal RNA gene Submitted (21-NOV-1995) Stefan Weidner, Fakultaet fuer Biologie, Lehrstuhl fuer Genetik, Universitaet Bielefeld, Universitaetsstr. 25, Bielefeld, D-33615, Germany Halophila stipulacea estimated by restriction fragment length polymorphism analysis of PCR-amplified 16S rRNA genes Appl. Environ. Microbiol. 62 (3), 766-771 (1996) unidentified marine eubacterium U41091 Weidner, S. Diversity of uncultured microorganisms associated with the seagrass Weidner, S., Arnold, W. and Puehler, A. Eubacteria. unidentified marine eubacterium g1293542 NCBI gi: 1293542 Direct Submission sequence. 10; ; O. (bases 1 to 956) (bases 1 to 956) 254 120 Conservative Conservative മ മ /gene="Hbx2" 371..427 Hyphomonas group" /product="165 ribosomal RNA" a 208 c 294 g 200 t <1..>956 /note="homeobox" 142..370 /note="related to 16S ribosomal /clone="HstpL6" note="associated with the seagrass Halophila stipulacea" organism="unidentified marine eubacterium" 1..956 Jocation/Qualifiers /note="homeobox" /gene="Hbx2" 'gene="Hbx2" 100 c Score 10; DB 82; Pred. No. 8.12e+02; Score 10; DB 84; Pred. No. 8.12e+02; 0; Mismatches 0; Mismatches 118 Q 9 4 0 0. Length 956; Length 427; RNAs Indels Indels from bacteria of the 0 0 Gaps Gaps <u>.</u> ç

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/note="associated with the seagrass Halophila stipulacea"
/clone="HstpL3" /product="16S ribosomal RNA" 209 c' 296 g 199 t /note="related to 16S ribosomal <1..>956 Location/Qualifiers 1..956 Location/Qualifiers marine 2060 bp eubacterium eubacterium. Score 10; DB 82; Pred. No. 8.12e+02; 0 Mismatches DB 82; Length 956; 0, RNAs from bacteria of the Indels 10-APR-1996 <u>.</u> Gaps 0;

> source US-08-644-289-5.rge

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exon /tissue\_type="placenta" 312..1938 /EC\_number="3.2.1.23" /gene="IGnT" organism="Homo sapiens"

enzyme" /codon\_start=1 /number=1 /note="Initiation codon starts at 1020; the I-branching

5'UTR intron /gene="IGnT" 1939..>2060 /product="beta-1,6-N-acetylglucosaminyltransferase" 312..1019

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Query Match Matches Query Match 100.0%; Best Local Similarity 100.0%; 10; Conservative Score Pred. 0; Mismatches 10; DB 90; No. 8.12e+02; 0 Length 2060; Indels 0; Gaps

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NID **LOCUS** ACCESSION DEFINITION RESULT H.sapiens mRNA for x85237 g899297 HSSF3A120 2613 bp splicing factor SF3a120 RNA 22-APR-1996

SOURCE KEYWORDS ORGANISM human. SF3a120 gene; splicing factor.

Homo sapiens Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Homo.

REFERENCE AUTHORS TITLE SURP family of proteins and is homologous to the essential splicing factor PRP21p of Saccharomyces cerevisiae Kramer, A., Mulhauser, F., Wersig, C., Groning, K. and Bilbe, G. Mammalian splicing factor SF3al20 represents a new member of the (bases 1 to 2613)

MEDLINE JOURNAL 96079958 RNA 1 (3), 260-272 (1995)

REFERENCE AUTHORS Kramer, A.J. 2 (bases 1 to 2613)

Submitted (09-MAR-1995) A.J. Kramer, Universite de Geneve, Dept de Biologie Cellulaire, 30 quai Ernest-Ansermet, 1211 Geneve 4, Direct Submission

Sequence overlapping with the SWITZERLAND one under the acc# T25051

COMMENT

NCBI gi: 899297

FEATURES source /evidence=experimental /gene="SF3a120" 98..2479 /note="NCBI gi: 899298" /codon\_start=1 'chromosome="22" /clone\_lib="lambda gt11" cell\_line="HeLa" organism="Homo sapiens" 1..2613 Location/Qualifiers

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                                                                      Catecholamine-sulfating phenol Biochem. Biophys. Res. Commun.
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                                      NCBI gi: 833898
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2237..2467
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SDDEVYAPGLDIESSLKQLAERRTDIFGVEETAIGKKIGEEEIQKPEEKVTWDGHSGS
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/db_xref="PID:g899298"
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Pred. No. 8.12e+02;
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                                                                          sulfotransferase gene (STM)";
205:1325-1332(1994).
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TITLE
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Sequence 3225 BP; 677 A; 940 C;
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                                                                                                                                                            NCBI
                                                                                                                                                                                                                                                                                                                                   Drosophila pseudoobscura
                                                                                                                                                                                                                                                                                                                                                               alcohol dehydrogenase; alternative splicing.
Drosophila pseudoobscura (sub_species bogotana)
                                                                                                                                                                                          Proc. Natl. Acad.
                                                                                                                                                                                                                                      Nucleotide sequence analysis of Adh genes estimates the time
                                                                                                                                                                                                                                                     Schaeffer, S.W. and Miller, E.L.
                                                                                                                                                                                                                                                                                                                                                   EMBL4)
                                                                                                                                                                                                                                                                                                                                                                                               g156855
                                                                                                                                                                                                                                                                                                                                                                                                                                alcohol dehydrogenase (adh) gene,
                                                                                                                                                                            91296768
                                                                                                                                                                                                        pseudoobscura
                                                                                                                                                                                                                      geographic isolation of the Bogota population of Drosophila
                                                                                                                                                                                                                                                                                    Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                    Tracheata; Insecta; Pterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DROADHBO39
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Similarity 100.0%;
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                                                                                                                                                         gi: 156855
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                                                                              /tissue_lib="EMBL4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPKSGTTWVSQILDMIYQGGDLEKCNRAPIYVRVPFLEVNDPGEPSGLETLKDTPPPR
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2959,3082..3194)
  /codon_start=1
8..14
                                 /number=1
                                               /note="unidentified reading frame"
                                                                                              /sub_species="bogotana
                                                                                                           /organism="Drosophila
                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKSHLP LALLPQTLLDQKVKVVYVARNPKDVAVSYYHFHRMEKAHPEPGTWDSFLEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MELIQDTSRPPLEYVKGVPLIKYFAEALGPLQSFQARPDDLLIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="PID:e163343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Description: catecholamine-sulfating phenol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="STM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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                                                                                                                                                                                          Sci.
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                                                                                                                                                                                       U.S.A. 88 (14), 6097-6101 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                             pseudoobscura"
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1467..1526
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TIAVNYTGLVNTTTA I LDFWDKRKGGPGGI I CNI GSVTGFNA I YQVPVYSGSKAAVVN
FTSSLAKLAP I TGVTAYTVNPGI TKTTLVHKENSWLDVEPRVAEKLLEHPTQTSQQCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="adh"
/note="adult"
                              /gene="adh"
2207..2507
/note="unidentified reading frame"
                                                                               /note="potential"
1942
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893..998
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join(860..998,1062..1466,1527..1942)
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1919..1924
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join(906..998,1062..1466,1527..1793)
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join(893..998,1062..1466,1527..1942)
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/note="larval"
                                                                                                                                                                                                                                                                                                                       1062..1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MSLTNKNVVFVAGLGGIGLDTSRELVKRNLKNLVILDRIDNPAA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="PID:g156856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="alcohol dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="NCBI gi: 156856"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="alcohol dehydrogenase"
120..892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
join(40..119,1062..1466,1527..1942)
               /number=1
                                                                                                                 /gene="adh"
                                                                                                                                                                  /number=3
                                                                                                                                                                                  'gene="adh"
                                                                                                                                                                                                    527..1942
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TITLE
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Best Local Similarity 100.0%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence analysis of Adh genes estimates the time of geographic isolation of the Bogota population of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 3463)
Schaeffer, S.W. and Miller, E.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosome IV, section 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila pseudoobscura (tissue library: EMBL4) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alcohol dehydrogenase; alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                       NCBI gi: 156821
                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6097-6101 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                              pseudoobscura
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                                                     /codon_start=1
join(40..119,1082..
/gene="adh"
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                                                                                                                                                                                                                                                                                              /organism="Drosophila
/tissue_lib="EMBL4"
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788 c 791 g 910 t
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2913..2970
/product="alcohol dehydrogenase" 120..912
                                       /note="adult"
                                                                                                                               ʻgene="adh"
                                                                                                                                                  40..119
                                                                                                                                                                                                                                          /number=i
                                                                                                                                                                                                                                                          /note="unidentified reading frame"
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                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                            note="adult"
                                                                                                                                                                  note="adult"
                                                                                                                                                                                     'gene="adh"
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Pred. No. 8.12e+02;
0; Mismatches 0;
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# Mar 25 02:55 US-08:644-289-5.rgc /note="potential; unidentified reading frame"

Mar 25 02:55

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
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                                                                                    BRNA
                                                                                                                                                      exon
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                                                                                                                                                                                                                                                                                                                                                                                promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \mathsf{g}156823 alcohol dehydrogenase; alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosome IV, section 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91296768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schaeffer, S.W. and Miller, E.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila pseudoobscura (tissue library: EMBL4) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI gi: 156823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6097-6101 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pseudoobscura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROADHAH15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 3465)
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Pred. No. 8.12e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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ORIGIN
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Best Local Similarity 100.0%;
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                             3321 aggcatgcct 3330
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Pred. No. 8.12e+02;
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                                                                                             Length 3465;
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FEATURES DEFINITION REFERENCE KEYWORDS ACCESSION AUTHORS TITLE MEDLINE JOURNAL ORGANISM exon SB mRNA exon mRNA exon mRNA exon intron promoter source g156825 M60987 Drosophila pseudoobscura Nucleotide sequence analysis of Adh genes estimates the time of geographic isolation of the Bogota population of Drosophila 1 (bases 1 to 3466) Schaeffer, S.W. and Miller, E.L. Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. alcohol dehydrogenase; alternative splicing. Drosophila pseudoobscura (tissue library: EMBL4) Drosophila pseudoobscura (strain AH162) alcohol dehydrogenase (adh) NCBI gi: 156825 gene, complete cds. Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6097-6101 (1991) pseudoobscura Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; DROADHAH16 1296768 /codon\_start=1
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COMMENT
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TITLE
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Schaeffer, S.W. and Miller, E.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI gi: 156831
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NID

g156831 M60988

gene, complete cds.

DEFINITION **LOCUS** 

Drosophila pseudoobscura (strain AH165) alcohol dehydrogenase (adh)

12

DROADHAH 6

3467 bp

DNA

WI

07-MAY-1996

SOURCE

alcohol dehydrogenase; alternative splicing.
Drosophila pseudoobscura (tissue library: EMBL4) DNA.
Drosophila pseudoobscura

ORGANISM

KEYWORDS ACCESSION မ 밁

10 AGGCATGCCT 1

ORIGIN

Chromosome IV, section 88

Query Match 100.0%; Best Local Similarity 100.0%;

Score 10; DB 83; Pred. No. 8.12e+02;

Length 3466;

0; Mismatches

Indels 0;

Gaps

0;

Matches

Conservative

3322 aggcatgcct 3331

BASE COUNT

973 a

/note="potential; unidentified reading frame"
1 788 c 793 g 912 t

g

polyA\_signal

/codon\_start=1 3357..3362

/number=3

/note="unidentified reading frame"

exon

/number=2 2987..>3347

/note="unidentified reading frame"

intron

2929..2986 /number=2

codon\_start=1

exon

2524..2928

'number=1

/note="unidentified

reading frame"

polyA\_site

polyA\_signal

/codon\_start=1 1950..1955

'number=3 'gene="adh" 547..1964 'number=2 'gene="adh"

Intron

/gene="adh" 2226..2523

/note="unidentified reading frame"

/note="potential" 1973

'gene="adh"

Mar 25 02-55

US-08-644-289-5.rgc

exon intron exon	intron	mRNA CDS	mRNA exon	intron	exon mRNA	exon promoter
/number=1 1083.1487 /gene="adh" /number=2 /codon_start=1 1488.1349 /gene="adh" /number=2 1550.1168 /gene="adh" /number=3 /codon_start=1	/ÉC_number="1.1.1.1" /note="NCB1 gi: 156852" /codon_start=1 /product="alcohol dehydrogenase" /bxref="pli:9158852" /db_xref="pli:9158852" /translation="MSLINKNVVFVAGLGGIGLDTSRELVKRNLKNLVILDRIDNPAA /translation="MSLINKNVVFVAGTGGIGLDTSRELVKRNLKNLVILDRIDNPAA /translation="MSLINKNVVFVAGTGKLLKTIFAQVKTIDVLINGAGILDDHQIER TIANNYTGLNNTTAILDFWDKRKGCPGGICNICNTGVTGYATYCSCKAAVVN FTSSLAKLAPITGVTAYTVNPGITKTTLVHKFNSWLDVEPRVAEKLLEHPTQTSQQCA ENFYKAAIELNKNGAIWKLDLGTLEPITWTQHWDSGI" 10211082 /gene="adh"	/codon start=1 join(9151020,10831487,15501968) /gene="adh" /note="adult" /product="alcohol dehydrogenase" join(9281020,10831487,15501816) /gene="adh"	/note="larval" /number=1 /codon_start=1 /codon_start=1 join(882120,10831487,15501968) /gene="adh" /note="larval" /product="alcohol_dehydrogenase" /product="adh" /note="adh"	<pre>/gene= adn /gene= adn! /note= adult /product= alcohol dehydrogenase 120914 /gene= adh /note= adult 882.1020 /gene= adh /gene= adh</pre>	/gene="adn" /note="adult" /note="adult" /note="adult" /codon start=1	

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RESULT
LOCUS
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                                                                                                                                                                                                                                                  AUTHORS
TITLE
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                                                                                                                                                                  NCBI
                                                                                                                                                                                                                               Nucleotide sequence analysis of Adh genes estimates the time geographic isolation of the Bogota population of Drosophila
                                                                                                                                                                                                                                                                                                                                                    Drosophila pseudoobscura
                                                                                                                                                                                                                                                                                                                                                                    Drosophila pseudoobscura (sub_species bogotana) EMBL4) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                alcohol dehydrogenase; alternative splicing.
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                                                                                                                                                                                                                                                                   Schaeffer, S.W. and Miller, E.L.
                                                                                                                                                                                                                                                                                                 Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                  Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 100.0%;
Similarity 100.0%;
                                                                                                                                                                                                                  pseudoobscura
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                                                                                                                                                                gi: 156843
                                                                                                                                                                                              Natl. Acad. Sci. U.S.A. 88 (14), 6097-6101 (1991)
                                                                                                                                1..3472
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1550..1965
/gene="adh"
/number=3
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join(883..1021,1085..1489,1550..1965)
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                                                                                                                      /codon_start=1
1942..1947
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1490..1549
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join(929..1021,1085..1489,1550..1816)
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join(9<mark>1</mark>6..1021,1085..1489,1550..1965)
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                                                                                                    "gene="adh"
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'db_xref="PID:g156844"
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                                                                                 note="potential"
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US-08-644-289-5.rgc

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RESULT 15
LOCUS DROADHAH10 3472 bp DNA INV 0/-ra....
DEFINITION Drosophila pseudoobscura (strain AH100) alcohol dehydrogenase adh gene, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DURCE Drosophila pseudoobscura (tissue library: EMBL4) DNA.
ORGANISM Drosophila pseudoobscura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3328 aggcatgcct 3337
                                                                           exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence analysis of {\tt Adh} genes estimates the time of geographic isolation of the Bogota population of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alcohol dehydrogenase; alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                  NCBI gi: 156815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schaeffer, S.W. and Miller, E.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6097-6101 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                         pseudoobscura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 3472)
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/tissue lib="FMBL4"
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2993..>3353
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polyA_signal		exon	intron	exon	intron	polyA_site	polyA_signal	exon		intron		exon		intron					CDS		exon		mRNA		HAWA.	T DAIN			exon	
33483353	<pre>/note="unidentified reading frame" /number=3 /codon start=1</pre>		/codon_start=1 29357992 /note="unidentified reading frame"	<pre>/number=1 25302934 /note="unidentified reading frame" /number=2</pre>	/gene- dum 2229.2529 /note="unidentified reading frame"	note="potential" 1964	1941.1946 1941.1946 /gene="adh"	1549.1964 (	/gene="adh"	/codon_start=1 1489.,1548	/ gene="adn" / number=2	10841488	/gene="adh" /number=1	10211083	IAELKAINPKVTITEYPYDVTVPVAETTKLLKTIFAQVKTIDVLINGAGILDDHQIER TIAVNYTGLUNTTAILDEWDKRKGGPGGIICNIGSVTGENAIYQVPVYSGSKAAVVN FTSSLAKLAPITGVTAYTVNPGITKTTLVHKENSMIDVEPRVAEKLLEHPTQTSQQCA ENTVKA FILKRIGA HKLDLGTLFP TTYTOHROSGI"	/db_xref="PID:g1303659" /translation="MSLTNKNVVFVAGLGGIGLDTSRELVKRNLKNLVILDRIDNPAA	/product="alcohol dehydrogenase"	/note="NCBI gi: 1303659"		/note="adult" /codon start=1		/note="adult" /product="alcohol dehydrogenase"	join(9151020,10841488,15491964) /gene="adh"	/note="larval" /product="alcohol dehydrogenase"	/gene="adh"	/codon_start=1	/note="larval" /number=1	/gene="adh"	/note="adult" 8821020	/gene="adh" /_ten="adh"

/note="potential; unidentified reading frame"
BASE COUNT 967 a 793 c 800 g 912 t
ORIGIN Chromosome IV, section 88. Query Match 100.0%; Score 10; DB 83; Length 3472; Best Local Similarity 100.0%; Pred. No. 8.12e+02; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3328 aggcatgcct 3337 ||||||||| Cp 10 AGGCATGCCT 1

Search completed: Tue Mar 25 02:57:03 1997 Job time : 55 secs.

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US-08-644-289-5.mg

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MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:57:21 1997; MasPar time 9.54 Seconds 91.416 Million cell updates/sec

Tabular output not generated.

Title: Perfect Score: Description: 10 (1-10) from US08644289.seq >US-08-644-289-5

N.A. Sequence: Comp: 1 AGGCATGCCT 10 TCCGTACGGA

Scoring table: TABLE default

Gap 10

Searched: Dbase 0; Query 0 113505 seqs, 43611913 bases x 2

Nmatch

STD :

Post-processing: Minimum Match 0%

Listing first 45 summaries

n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22

Statistics: Mean 4.316; Variance 1.934; scale 2.231

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

C	ი	a				G		Result No.
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10	10	10	10	10	10	10	10	No. Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
20	20	20	20	20	20	10	10	Query Match Length DB
19	5	21	5	21	19	5	5	DB.
T10102	Q31978	T15968	Q31978	T15968	T10102	Q31948	Q31948	ij
Human cholecystokinin	Synthetic oligomer 4,	Primer for human CCK-	Synthetic oligomer 4,	Primer for human CCK-	Human cholecystokinin	Monomeric p53-specifi	Monomeric p53-specifi	Description
			1.99e+02				1.99e+02	Pred. No.

C	C	C	O				C	O			C		C		C		a		O				O	O		O		C		ဂ		C			
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100.0	•	100.0		100.0						100.0							100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	٠	100.0	100.0	100.0	100.0	100.0	100.0	100.0	8		
4839	3353	3353	3353	3353	3353	3353	3102	3102	3102	3102	2754	2754	2272	2272	2136	2136	1969	1969	1807	1807	1807	1416	831	265	265	91	91	46	46	42	42	24	24	24	24
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006827	204496	Q54258	N81234	Q14097	Q54258	Q04496	Q10402	Q56931	Q10402	Q56931	T14603	T14603	T11104	T11104	Q64563	Q64563	Q47671	Q47671	Q89201	Q89201	T16201	Q96290	Q79912	Q47710	Q47710	Q51746	Q51746	Q31958	95	3	Q80759	T11108	Q47714	$\mathbf{H}$	ROTILI
Alpha amylase pullula Alpha amylase pullula	nce of g	pre	of human	precursor	Amyloid precursor pro	Sequence of gene enco	Insert DNA of pGP130	Human soluble glycopr		soluble glyco	gp130 native	Human gp130 native ge		orming	₩	B		the hun		I-branching enzyme cD	-N-acetylglu	Partial sequence of b		beta-like clone	TGF-beta-like clone M		onucleotide prol	binding site of		Pilot oligonucleotide	ucleotid	growth	e clone		Transforming growth f
1.99e+02 1.99e+02							1.99e + 02		1.99e+02			1.99e+02	1.99e+02			1.99e+02	1.99e+02	1.99e+02	1.99e+02	•	1.99e+02		1.99e+02		•	•	•				1.99e+02			96	1.99e+02

#### ALI GNMENTS

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RESULT
chemotherapeutic agents
Claim 22; Page 24; 51pp; English.
Claim 25; Page 24; 51pp; English.
Wild-type p53 protein binds specific fragments of human chromosomal
DNA. Each fragment contains no more than one monomer of the double
DNA. Each fragment contains no more than one monomer of the double
                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1992.
10-JUN-1992; 305333.
14-JUN-1991; US-715182.
31-MAR-1992; US-860758.
                                                                                                                                                                                                                 Detection and expression of wild type P53 protein - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P53; DNA-binding; cancer; neoplasia; tumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q31948;
27-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q31948 standard; DNA; 10 BP
                                                                                                                                                                                      diagnosing and treating cancers, and for screening potential
                                                                                                                                                                                                                                                    WPI; 92-417505/51.
                                                                                                                                                                                                                                                                             Kinzler KW, Sherman MI, Vogelstein B;
                                                                                                                                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                      (PHAR-) PHARMAGENICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP-518650-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monomeric p53-specific DNA binding site.
                                        one monomer of the double base pairs. Some of these
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commonly found in human tumours do not have the ability to bind to

viruses and animal cells. Four mutant forms of p53 protein which are sequences are found near the origin of replication of certain animal

Mar 25 02:55

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allows identification of wild type p53, and such a construct could
be used for diagnosis of p53 mutations and onset and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  these sequences. Thus a function of p53 may be mediated by its ability to bind specific DNA sequences in the human genome. The sequence shown is a consensus sequence for p53 DNA binding. When
                    restored to neoplastic cells having a mutation in their p53 gene. See also Q31949-84.
                                                                                                                                                                                                                                                                                          DNA. Each fragment contains no more than one monomer of the double stranded sequence shown separated by 0-13 base pairs. Some of thes
                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYJO ) UNIV JOHNS HOPKINS.
Kinzler KW, Sherman MI, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P53; DNA-binding; cancer; neoplasia; tumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q31948 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restored to neoplastic cells having a mutation in their p53 gene. See also 031949-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bind p53-specific DNA. Also wild-type p53 gene function may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chemotherapeutic agents and to identify agents which specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              various cancers. The construct may also be used to screen potential
                                                        bind p53-specific DNA. Also wild-type p53 gene function may be
                                                                            chemotherapeutic agents and to identify agents which specifically
                                                                                              various cancers. The construct may also be used to screen potential
                                                                                                                  be used for diagnosis of p53 mutations and onset and development of
                                                                                                                                 inserted upstream and adjacent to a reporter gene the sequence allows identification of wild type p53, and such a construct could
                                                                                                                                                                       ability to bind specific DNA sequences in the human genome. The sequence shown is a consensus sequence for p53 DNA binding. When
                                                                                                                                                                                                              these sequences. Thus a function of p53 may be mediated by
                                                                                                                                                                                                                                  viruses and animal cells. Four mutant forms of p53 protein which are commonly found in human tumours do not have the ability to bind to
                                                                                                                                                                                                                                                                      sequences are found near the origin of replication of certain animal
                                                                                                                                                                                                                                                                                                                                  Wild-type p53 protein binds specific fragments of human chromosomal
                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 24; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                       chemotherapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                         diagnosing and treating cancers,
                                                                                                                                                                                                                                                                                                                                                                                                             Detection and expression of wild type P53 protein - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 92-417505/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PHAR-) PHARMAGENICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1992; US-860758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-1991; US-715182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1992; 305333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP-518650-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monomeric p53-specific DNA binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q31948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inserted upstream and adjacent to a reporter gene the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-1992.
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0 A;
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Pred. No. 1.99e+02;
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1 C;
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1 G;
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0 U;
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                                                                                                                                                                                                                                                                                                                                                                                         potential
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Best Local Similarity 100.0%;
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Best Local Similarity 20.0%;
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                                                                                                                                                                          gastric secretion; tranquilizer; assay; production; primer; PCR,
                                                                                                                                                                                                         09-SEP-1996 (first entry)
Primer for human CCK-B/gastrin receptor gene amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 7; 14pp; Japanese.

A cDNA sequence encoding the human isoform of cholecystokinin-B/
gastrin receptor was isolated (see T10094). The present sequence is
that of a PCR primer which was used in cloning the full-length cDNA.
                                            WPI; 96-136331/14.
                                                                                                                                                                                              CCK-B/gastrin; cholecystokinin-B/gastrin receptor; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               candidate antagonists of the receptor. Such antagonists have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cells transformed with the human coding sequence will express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cholecystokinin-B/gastrin receptor protein and gene - used to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 96-065478/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-1994; JP-117015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antagonist; gastric acid secretion; inhibition; anti-anxiety; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholecystokinin B; CCK-B; gastrin; receptor; human; isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cholecystokinin-B/gastrin receptor PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T10102 standard; DNA; 20 BP.
             develop antagonists used to evaluate inhibitors of gastric acid
                             Gene encoding cholecystokinin-B/gastrin receptor - useful, e.g. to
                                                                             22-JUL-1994; 170663.
22-JUL-1994; JP-170663.
                                                                                                                                                              polymerase chain reaction;
                                                                                                                                                                                                                                                              T15968 standard; cDNA to mRNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anxiety agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                potential use as inhibitors of gastric acid secretion or as anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor on their surface and will thus be useful for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-anxiety agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and evaluate agents for use as gastric acid secretion inhibitors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T10102;
                                                                                                               30-JAN-1996.
                                                                                                                                J08027190-A.
                                                                                                                                                Synthetic.
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                                                             (YAMA ) YAMANOUCHI PHARM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2-DEC-1995.
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                                                                                                                                                              amplification; ss.
                                                               G.T.T
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Pred. No. 1.99e+02;
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Pred. No. 1.99e+02;
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                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 T;
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                                                                    Matches
                                                                                    Best Local
                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 7; 15pp; Japanese.
T15963-68 were used to PCR amplify a DNA fragment contg. a human cholecystokinin-B/gastrin receptor gene (see T15960). Host cells transformed with the gene are useful for recombinant production of the receptor protein. The receptor is useful for the development of
                                                                                                                                                                                                                                                                                                                            The sequences of these 23 clones was compared and an average insert of 307 bp (range 139-470) was found. Only 18 of the clones contained unique fragments. Alignment of the inserts revealed a striking and
                                                                                                                                                                                      motif is required to bind p53, that G residues at nucleotides 4 and 6 are critical for p53 binding and that mutant p53 proteins found in tumours do not bind to the consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                  Wild-type p53 protein binds specific fragments of human chromosomal DNA. 23 clones which bound p53 were obtd. by whole genome PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid secretion and tranquilizers, etc... Sequence 20 BP; 4 A; 6 C; 4 (
                                                                                                                                                                                                                                         were synthesised to determine portions of the motif vital for p53 binding. Mutation analysis revealed that the dimer of the consensus
                                                                                                                                                                                                                                                                              consensus sequence contains internal symmetry.
                                                                                                                                                                                                                                                                                               consistent feature, each binding site contained two copies of the 10\ \mathrm{bp}\ \mathrm{motif}\ 5'-\mathrm{RRRCWHGYYY-3'} separated by 0-13\ \mathrm{bp}. The 10\ \mathrm{bp}
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 10; Fig 10; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing and treating cancers, and for screening potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinzler KW, Sherman MI, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P53; DNA-binding; cancer; neoplasia; tumour; concatemer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic oligomer 4, to determine motif for binding to p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q31978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q31978 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical drugs, esp. antagonists to evaluate inhibitors of gastric
                                                                                                                                                       See also Q31948-84.
                                                                                                                                                                      Oligonucleotide 4 was capable of binding
                                                                                                                                                                                                                                                                                                                                                                                                                                      chemotherapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection and expression of wild type P53 protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHAR-) PHARMAGENICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1992; US-860758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP-518650-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 100.0%;
Local Similarity 100.0%;
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 aggcatgcct 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGCATGCCT 10
                                  aggcatgcct 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92-417505/51.
 AGGCATGCCT 10
                                                                                   h 100.0%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                  Conservative
                                                                                                                                       ₽,
                                                                                                                                    4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽P
                                                                                    Pred.
                                                                                                   Score 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                       6 C;
                                                                  <u>,</u>
                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; DB 21;
                                                                                    No. 1.99e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 G;
                                                                                                                                     6 G;
                                                                                                     DB 5;
                                                                                                                                                                         p53.
                                                                                                                                     4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 T;
                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                  <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                              Synthetic oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                    Indels
                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>,</u>
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                               The sequences of these 23 clones was compared and an average insert of 307 bp (range 139-470) was found. Only 18 of the clones contained unique fragments. Alignment of the inserts revealed a striking and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceuticar uray, ... acid secretion and tranquilizers, etc...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer for human CCK-B/gastrin receptor gene amplification.
                                   consistent feature, each binding site contained two copies of the
                                                                                                                    Wild-type p53 protein binds specific fragments of human chromosomal
                                                                                                                                                  chemotherapeutic agents
                                                                                                                                                                      diagnosing and treating cancers, and
                                                                                                                                                                                                         WPI; 92-417505/51.
                                                                                                                                                                                                                                       (PHAR-) PHARMAGENICS INC. (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                         14-JUN-1991; US-715182.
31-MAR-1992; US-860758.
                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                            P53; DNA-binding; cancer; neoplasia; tumour; concatemer;
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic oligomer 4, to determine motif for binding to p53.
                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Q31978;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q31978 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical drugs, esp. antagonists to evaluate inhibitors of gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor protein. The receptor is useful for recombinant production of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastric secretion; tranquilizer; assay; production; primer; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCK-B/gastrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-1996 (first entry)
                                                                                                                                    Example 10; Fig 10; 51pp; English.
                                                                                                                                                                                      Detection and expression of wild type P53 protein - useful for
                                                                                                                                                                                                                       Kinzler KW, Sherman MI, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                             EP-518650-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholecystokinin-B/gastrin receptor gene (see T15960). Host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             develop antagonists used to evaluate inhibitors of gastric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene encoding cholecystokinin-B/gastrin receptor - useful,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1994; JP-170663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymerase chain reaction; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T15968
                 10 bp motif 5'-RRRCWWGYYY-3' separated by 0-13 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1994; 170663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J08027190-A.
                                                                                                                                                                                                                                                                                                            10-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [15963-68 were used to PCR amplify a DNA fragment contg. a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 7; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AGGCATGCCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 aggcatgcct 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96-136331/14.
                                                                                                   23 clones which bound p53 were obtd. by whole genome PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
sequence contains internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cholecystokinin-B/gastrin receptor; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10; DB 21;
Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                    for screening potential
 symmetry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                 The 10 bp
 oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.
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PSEEDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                    Query Match
                                           Transforming growth factor beta cDNA clone MP-121 PCR primer IO2. TCF-beta; MP-121; mitogen; differentiation; induction; promotion; maintenance; morphogen; tissue regeneration; dental implantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and 6 are critical for p53 binding and that mutant p53 proteins found in tumours do not bind to the consensus sequence.
                                                                                                                                                                                                                                                                                                                                candidate antagonists of the receptor. Such antagonist potential use as inhibitors of gastric acid secretion
                                                                                                                                                                                                                                                                                                                                                               Cells transformed with the human coding sequence will express the receptor on their surface and will thus be useful for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic. 
J07324099-A.
                Synthetic.
                                                                                            09-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                gastrin receptor was isolated (see T10094). The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                               A cDNA sequence encoding the human isoform of cholecystokinin-B/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and evaluate agents for use as gastric acid secretion inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cholecystokinin-B/gastrin receptor protein and gene - used to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 96-065478/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonist; gastric acid secretion; inhibition; anti-anxiety; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cholecystokinin B; CCK-B; gastrin; receptor; human; isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cholecystokinin-B/gastrin receptor PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T10102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also Q31948-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide 4 was capable of binding p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               motif is required to bind p53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              were synthesised to determine portions of the motif vital for p53
 DE19511243-A1.
                             wound healing; polymerase chain reaction; PCR primer; ss.
                                                                                                                        T11108 standard; cDNA;
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                 anxiety agents.
                                                                                                                                                                                                                                                                                                                                                                                                that of a PCR primer which was used in cloning the full-length cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 7; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                antı-anxiety agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-1994; JP-117015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-1994; 117015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T10102 standard; DNA;
                                                                                                                                                                                                                                                     Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 aggcatgcct 10
                                                                                                                                                                                                     7 aggcatgcct 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGCATGCCT 1
                                                                                                                                                                         AGGCATGCCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutation analysis revealed that the dimer of the consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 BP;
                                                                                                                                                                                                                                                                                                     20 BP;
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 A;
                                                                                                                                                                                                                                                                                                   4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                           24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽₽
                                                                                                                                                                                                                                                       Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                    Score 10; DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 C;
                                                                                                                                                                                                                                                                                                   6 C;
                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that G residues at nucleotides 4
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 1.99e+02;
                                                                                                                                                                                                                                                                                                   4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                 Such antagonists have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 T;
                                                                                                                                                                                                                                                                                                   6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                    as anti-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                      Gaps
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## Mar 25 02:55 US-08-644-289-5.mg

Ş 맑 Matches Query Match coding for a TGF-beta-like protein was isolated. The protein encoded Example 1; Page 6; 15pp; German. A cDNA library prepared using total RNA from human liver was 04-JAN-1996. 27-MAR-1995; 011243. Transforming growth factor beta cDNA clone MP-121 internal primer TGF-beta; MP-121; mitogen; differentiation; induction; promotion; maintenance; morphogen; tissue regeneration; dental implantation; T11107 standard; cDNA; 24 BP. properties making it (or fusion proteins comprising it or heterodimers of the protein with a cystine knot motif protein) useful for inducing tissue regeneration. The present sequence is that of a PCR primer by the cDNA insert has mitogenic and differentiation-inducing to contain a new sequence. Part of the insert from this clone was A cDNA library prepared using total RNA from human liver was and differentiation-inducing activity, e.g. for use in Bechtold R, 01-JUL-1994; DE-423190. properties making it (or fusion proteins comprising it or heterodimers by the cDNA insert has mitogenic and differentiation-inducing used to re-screen the human liver cDNA library and a 2272 bp fragment to contain a new sequence. Part of the insert from this clone was regions within the TGF-beta family. Amplification products were subjected to PCR amplification using primers corresp. to conserved and differentiation-inducing activity, e.g. for use in DNA encoding transforming growth factor beta MP-121 - has mitogenic WPI; 96-050788/06. Bechtold R, 01-JUL-1994; DE-423190. DE19511243-A1. Synthetic wound healing; polymerase chain reaction; PCR primer; ss. 09-AUG-1996 (first entry) Sequence amplification using primer LO2 (i.e. this sequence) and primer LOI1 human liver library; positive clones were then subjected to PCR based on a DdeI fragment comprising nucleotides 931-1304 of the coding for a TGF-beta-like protein was isolated. The protein encoded used to re-screen the human liver cDNA library and a 2272 bp fragment subcloned and sequenced; one clone (designated pSK-MP121) was found regions within the TGF-beta family. Amplification products were subjected to PCR amplification using primers corresp. to conserved Example 1; Page 6; 15pp; German. DNA encoding transforming growth factor beta MP-121 - has mitogenic WPI; 96-050788/06. (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL subcloned and sequenced; one clone (designated pSK-MP121) was found (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL. 2272 bp insert. The DdeI fragment was used as a probe to screen the 27-MAR-1995; 011243. (see T11109). Local 8 aggcatgcct 17 AGGCATGCCT 10 10; h 100.0%; Similarity 100.0%; Neidhardt H, Neidhardt H, Conservative ₽, 6 A; Pohl J, Pohl J, Score 10; DB 20; Pred. No. 1.99e+02; 5 C; Mismatches Hoetten G; Hoetten G; 7 G; 6 T; <u>.</u> Length Indels 24 wound healing wound ٥, primer. healing Gaps <u>,</u>

US-08-644-289-5.mg

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RESULT
ID T:
AC T:
DT 00
DT T:
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                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the protein with a cystine knot motif protein) useful for ind tissue regeneration. The present sequence is that of an internal primer which was used for isolating the cDNA coding sequence.
                             Transforming growth factor beta cDNA clone MP-121 PCR primer IO2. TGF-beta; MP-121; mitogen; differentiation; induction; promotion; maintenance; morphogen; tissue regeneration; dental implantation;
                                                                                                                                                                                                                                                                                                                                                               for the treatment of various bone, cartilage or tooth defects and in
tissue and wound repair processes. These proteins may also be used
as immunosuppressors in organ transplants and in cosmetic surgery.
                                                                            09-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in 047711-14 are primers which may be used in the amplification of the liver derived human transforming growth factor-beta (TGF-beta) clone MP-121. The ampification product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
 Synthetic.
                                                                                                  T11108;
                                                                                                              T11108 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                 encodes a protein which may be used in a pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in tissue and wound repair, in treatment of bone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transforming growth factor-beta family proteins and DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organ transplant; cosmetic surgery; antibody; diagnosis; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone; cartilage; tooth; wound repair; immunosuppressor; PCR; amplify;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q47714 standard;
               wound healing; polymerase chain reaction; PCR primer;
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                   purposes.
                                                                                                                                                                                                                                                                                                                                                   Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 13; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and tooth defects, and antibodies for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-272824/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoetten G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9316099-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGF-beta-like clone MP-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-FEB-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-1992; EP-102324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-1993; E00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-AUG-1993.
                                                                                                                                                                                                                                                               Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                                                                                8 aggcatgcct 17
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                                                                                                                                                                                 AGGCATGCCT 10
                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                  24 BP;
                                                                                                                                                                                                                                                                                                                                                 raised against these proteins may be used for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neidhardt H;
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                cDNA; 24 BP.
                                                                                                                                                                                                                                                                                                                6 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cystine knot motif protein) useful for inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolating the cDNA coding sequence.
5 C; 7 G; 6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      internal nested primer.
                                                                                                                                                                                                                                                                Score 10; DB 8; L
Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10; DB 20;
                                                                                                                                                                                                                                                                                                                  5 c;
                                                                                                                                                                                                                                                 <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                7 G;
                                                                                                                                                                                                                                                                                                                  6 T;
                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                              Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                    composition
                                                                                                                                                                                                                                                 <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                 <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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မှ 밁 Matches Best Local Query Match by the cDNA insert has mitogenic and differentiation-inducing properties making it (or fusion proteins comprising it or heterodimers of the protein with a cystine knot motif protein) useful for inducing of the protein with a cystine knot motif protein) useful for inducing of the protein with a cystine knot motif protein useful for inducing subcloned and sequenced; one clone (designated pSK-MP121) was found to contain a new sequence. Part of the insert from this clone was used to re-screen the human liver cDNA library and a 2272 bp fragment coding for a TGF-beta-like protein was isolated. The protein encoded subjected to PCR amplification using primers corresp. to conserved A cDNA library prepared using total RNA from human liver was 27-MAR-1995; 011243. 01-JUL-1994; DE-423190. Sequence amplification using primer LO2 (i.e. this sequence) and primer LOI1 human liver library; positive clones were then subjected to PCR based on a DdeI fragment comprising nucleotides 931-1304 of the regions within the TGF-beta family. Amplification products were Example 1; Page 6; 15pp; German. and differentiation-inducing activity, e.g. for use in wound healing DNA encoding transforming growth factor beta MP-121 - has mitogenic Bechtold R, 04-JAN-1996. DE19511243-A1. 2272 bp insert. The DdeI fragment was used as a probe to screen the (see Tlll09). Sequence 24 (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL. 10 8 aggcatgcct 17 AGGCATGCCT 1 Similarity 100.0%; 10; Neidhardt H, Conservative ₽₽; 100.0%; 6 A; Pohl Score 10; DB 20; Pred. No. 1.99e+02; 5 c; ŗ Mismatches 7 G; Hoetten ٠. 6 T; Length 24; Indels 9 Gaps 0

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RESULTI
ID 08
AG 0
hybridizes to substrate RNA. Sequence 42 BP; 8 A;
                                                                                                                                                                                                                                                                                                   Disclosure; Page 98; 159pp; English.
The ability of a 5' nuclease to cleave a specific sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brow MAD, Dahlber WPI; 95-036504/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pilot oligonucleotide 30-12.

DNA-polymerase; DNAP; 5' nuclease; Thermus; DNA cleavage;
RNA cleavage; transcleavage; pilot oligonucleotide; hairpin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q80759 standard; DNA; 42 BP
                                                                                                  tetra-loop, and pilot oligonucleotide
                                                                                                                                                    substrate DNA to create a short hairpin with a stabilizing
                                                                                                                                                                                                          structure was tested using the pilot oligonucleotides 19-12 (given in Q80758) and 30-12 (Q80758), which hybridize to
                                                                                                                                                                                                                                                                                                                                                                                                                          detection of specific target sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cleavage activity with reduced synthetic ability, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUN-1993; US-073384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9429482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q80759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1994; U06253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclease(s) derived from thermostable DNA polymerase(s) eavage activity with reduced synthetic ability, used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dahlberg JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyamichev VI;
    12 C;
    12 G;
                                                                                                  30-0 (080760),
    10 T;
                                                                                                       which
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have

S

1 AGGCATGCCT 10

밁

23 aggcatgcct 32

Query Match 100.0%; Best Local Similarity 100.0%;

Score 10; DB 13; Pred. No. 1.99e+02;

DB 13; Length

Mismatches

U; Indels

0

Gaps

0

10;

Conservative

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RESULT
110 03
AC 03
AC 03
AC 03
DT 27
DE P5
KW P5
KW P6
KW P7
KW P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
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Nuclease(s) derived from thermostable DNA polymerase(s) - have cleavage activity with reduced synthetic ability, used for detection of specific target sequences.

Disclosure; Page 98; 159pp; English.

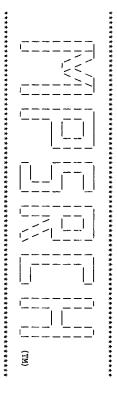
The ability of a 5' nuclease to cleave a specific sequence.
                                                                                                                                                                                                                                                                                                                                                                                         Q31958 standard; DNA; 46 BP.
Q31958;
Q7-APR-1993 (first entry)
P53 binding site of cloned human genomic fragment W211.
P53; DNA-binding; cancer; neoplasia; tumour; concatemer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pilot oligonucleotide 30-12.

DNA-polymerase; DNAP; 5' nuclease; Thermus; DNA cleavage;
RNA cleavage; transcleavage; pilot oligonucleotide; hairpin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   080759;
  14-JUN-1991;
31-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure was tested using the pilot oligonucleotides 19-12 (given in Q80758) and 30-12 (Q80758), which hybridize to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q80759 standard; DNA; 42
                                                                                                                            EP-518650-A.
                                                                                                                                              /*tag= b
/note= "homology with consensus p53 binding site"
                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                 /note= "homology
                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tetra-loop, and pilot oligonucleotide 30-0\ (Q80760), which hybridizes to substrate RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substrate DNA to create a short hairpin with a stabilizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (THIR-) THIRD WAVE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                               10-JUN-1992; 305333.
                                                                                            16-DEC-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dahlberg JE, Lyamichev VI;
; US-715182.
; US-860758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-073384.
                                                                                                                                                                                                                 / with consensus p53 binding site*
26..31
                                                                                                                                                                                                                                                                                                           Location/Qualifiers 16..25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      뫋
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 10; DB 13; I
Pred. No. 1.99e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 C;
                                                                                                                                                                                                                                                                                                                                                                                                        tumour; concatemer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Job time : 14 secs.

Search completed: Tue Mar 25 02:57:35 1997

δ В Matches Query Match 100.0%; Best Local Similarity 100.0%; Sequence consensus sequence contains internal symmetry. Mutation analysis revealed that the dimer of the consensus motif is required to bind p53 and that mutant p53 proteins found in tumours do not bind to the consistent feature, each binding site contained two copies of the 10 bp motif 5'-RRRCWWGYYY-3' separated by 0-13 bp. The 10 bp DNA. 23 clones which bound p53 were obtd. by whole genome PCR. chemotherapeutic agents Detection and expression of wild type P53 protein – useful for diagnosing and treating cancers, and for screening potential  ${\bf r}$ consensus sequence. See Sequence 46 BP; 6 A; unique fragments. Alignment of the inserts revealed a striking and of 307 bp (range 139-470) was found. Only 18 of the clones contained The sequences of these 23 clones was compared and an average insert Wild-type p53 protein binds specific fragments of human chromosomal Example 10; Fig 10; 51pp; English. Kinzler KW, Sherman MI, Vogelstein
WPI; 92-417505/51. (PHAR-) (UYJO) 16 aggcatgcct 25 AGGCATGCCT 10 UNIV JOHNS HOPKINS. PHARMAGENICS 10; Conservative See also Q31948-84. Score 10; DB 5; L Pred. No. 1.99e+02; 16 C; 0; Mismatches В 6 G; 0; Indels Length 46; 18 T; 0; Gaps 0



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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:57:55 1997; MasPar time 54.05 Seconds 81.591 Million cell updates/sec

Tabular output not generated.

N.A. Sequence: Description: Perfect Score: Title: 10 (1-10) from US08644289.seq >US-08-644-289-5 1 AGGCATGCCT 10

Scoring table: TABLE default

Comp:

TCCGTACGGA

Gap

Nimatch STD: Dbase 0; Query 0 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: :EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8

9:EST9 10:EST10 11:EST11

12:EST12 13:EST13 14:EST14

15.EST15 16.EST16 17.EST17 18.EST18 19.EST19 20.EST20 21.EST27 22.EST27 24.EST2 23.EST20 27.EST27 28.EST25 26.EST26 27.EST27 28.EST26 29.EST29 30.EST30 31.EST31 32.EST32 33.EST33 34.EST34 35.EST35 36.EST36 37.EST37 38.EST38 39.EST39 40.EST40 41.EST41 42.EST42 43.EST43 44.EST44 45.EST45 46.EST46 47.EST47 48.EST48 49.EST49 50.EST50 51.EST51 52.EST55 53.EST53 54.EST56 61.EST61 62.EST66 67.EST57 58.EST58 59.EST59 60.EST66 67.EST67 68.EST68 69.EST67 79.EST77 71.EST77 72.EST77 73.EST73 74.EST74 75.EST75 76.EST76 71.EST77 78.EST78 79.EST79 39.EST98 89.EST98 90.EST99 91.EST91 92.EST99 93.EST99 94.EST94 95.EST96 97.EST97 98.EST98

EST-STS-TWO 99:EST99

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100:EST100 101:EST101 102:EST102 103:EST103 104:EST104 105:EST105 106:EST106 107:EST107 108:EST108 109:EST009 110:EST110 111:EST111 112:EST112 113:EST113 114:EST114 115:EST115 116:EST116 117:EST117 118:EST118 119:EST119 120:EST120 121:EST121 122:EST122 123:EST123 124:EST124 125:EST125 126:EST126 127:EST127 128:EST128 129:STS1

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130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7 136:STS8 137:STS9 138:STS10 139:weEST 140:gnEST1 141:gnEST1 142:gnEST3 143:gnEST4 144:gnEST5 145:gnEST6 146:gnEST7 147:gnEST8 148:gnEST9 149:gnEST10 150:gnEST11 151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST15 152:gnEST13 153:gnEST14 154:gnEST2 159:enEST3 155:gnEST16 156:gnST5 157:enEST1 158:enEST2 159:enEST3 156:enEST4 161:enEST5 162:enEST1 168:enEST7 164:enEST8 166:enEST9 166:enEST10 167:enEST1 168:enEST1 168:enEST10 167:enEST1 168:enEST1 168:enEST10 166:enEST10 173:enSTS1 174:enSTS2 [69:enEST13 170:enEST14 171:enEST15 172:enEST16

Statistics: Mean 5.340; Variance 0.849; scale 6.287

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., za96h06.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 300443
5' similar to contains LTR5.t3 LTR5 repetitive element ;. 27-APR-1996 (Rel. 47, Created) 27-APR-1996 (Rel. 47, Last, updated, Key Hillier L., W07128; HS128324 Sequence source stop: 110. NCBI gi: 1281421 further information. Seq primer: mob.REGA+ET High quality sequence Contact: Wilson RK WashU-Merck EST Project Washington University Unpublished Theria; Eukaryota; Homo sapiens (human) LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) "The WashU-Merck EST Project"; Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; ta; Animalia; Metazoa; Chordata; Eutheria; Primates; Haplorhini; 205 standard; RNA; EST; ₽P ; /clone\_lib="Soares fetal lung NbHL19W"
/dev\_stage="19 weeks"
/lab\_host="DH10B (ampicillin resistant)" Soares and M.Fatima Bonaldo. This library was constructed adapters (Pharmacia), digested with Not I and cloned into /clone="300443" fetal heart NbHH19W. normalization to a Cot = 5. Library constructed by Bento (Pharmacia). Library went through one round of the Not I and Eco RI sites of a modified pT7T3 vector /organism="Homo sapiens" 58 A; 49 C; 53 G; 42 T; 3 other; from the same fetus as the fetal heart library, Soares Location/Qualifiers 205 BP Version 1) ; Vertebrata; ; Catarrhini; Length 205; Mammalia; Hominidae. Marra M., for

Matches Query Match 100.0%; Best Local Similarity 100.0%; 71 aggcatgcct 80 10; Conservative Score 10; DB 158; Pred. No. 2.46e+01; 0; Mismatches 0 Indels <u>.</u> Gaps 0

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AGGCATGCCT 10

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SOURCE NID RESULT Ş 밁 FEATURES COMMENT REFERENCE REFERENCE UN TOCUS KEYWORDS ACCESSION DEFINITION Locus BASE COUNT SOURCE KEYWORDS ACCESSION DEFINITION Query Match 100.0%; Best Local Similarity 100.0%; ORGANISM Matches JOURNAL AUTHORS AUTHORS ORGANISM JOURNAL source 129 aggcatgcct 138 <u>--</u> AGGCATGCCT 10 gl178126 EST(expressed sequence tag); Human fetal brain. Homo sapiens Fetus brain cDNA to mRNA, clone\_lib:human fetal brain. Homo sapiens  $% \left( 1\right) =\left\{ 1\right\} =\left$ D80249 Human fetal brain cDNA 5'-end GEN-052G06 Human fetal EST(expressed sequence tag); Human fetal brain. g1178126 HUM052G06B 463-10 Kagasuno Kawauchi-cho 0tsuka Otsuka GEN Research Institute Unpublished (1995) Maekawa, H., Shin, S. and Nakamura, Y. Okuno, S., Ozaki, K., Shimizu, F., Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Co., Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Direct Submission Fujiwara, T. D80249 HUM052G06B Vertebrata; Eutheria; Primates; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 10; Fax :0886-37-1035 Phone:0886-65-2888 771-01 Tokushima, Tsutomu Fujiwara Submitted (7-Nov-1995) to DDBJ Large-scale sequencing project at Otsuka GEN Research Institute Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., υapan Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; (bases 1 to 239) (bases 1 to 239) 5 Conservative Pharmaceutical CO., Ltd /organism="Homo sapiens"
/sequenced\_mol="cDNA to mRNA"
/tissue\_type="brain"
58 c 55 g 44 t /clone\_lib="human fetal brain" /dev\_stage="Fetus" Location/Qualifiers Tokushima 239 bp brain cDNA 239 bp Score 10; DB 46; Pred. No. 2.46e+01; <u>,</u> mRNA E 5'-end GEN-052G06. iiRNA Mismatches by: Catarrhini; Hominidae; Shimada, Y., Shinomiya, H., 0 Length 239; 17 others Indels 18-DEC-1995 18-DEC-1995 Hirai, Y., 0; Homo. fetal brain. Gaps 0

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                                                                                                i (bases 1 to 255)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
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                                                           Theising, B., Wylie, T., Lennon, G., Soares, B., Waterston, R.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                   Unpublished (1995)
                                                                                               Hudson, T.
                                                                                                                                                      Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
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Contact: Thomas Hudson
                                                        Mapped STSs
                                                                            Whitehead Institute/MIT Center for Genome Research; Physically
                                                                                                                                       Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                  (bases 1 to 269)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares mouse p3NMF19.5"
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                                                                                                                                                                                                                                                                                                                                      269 bp
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Pred. No. 2.46e+01;
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Whitehead Institute/MIT Center for Genome Research

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Best Local Similarity 100.0%;
              HSA244WH5 standard; DNA; STS; 272 BP. 252679; 18-MAR-1996 (Rel. 47, Created) 23-MAR-1996 (Rel. 47, Last updated, Version 3)
H.sapiens (D1S2675)
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9 Cambridge Center, C
Tel: 617 252 1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tris-HCL: 10 mM pH: 9.3
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KCl: 50 mM
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                                                                                                                                                                                                                                                                                                                            /map="746 D 8; 854 E 5; 891 G 9; 950 G 3; 950 G 4;
747 D 11; 811 D 12; 848 C 10; 854 E 10; 870 G 10; 730.7 cR
from top of Chrl linkage group"
13 c 66 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                        /map="746_D_8; 854_E_5; 891_G_9; 950_G_3; 950_G_4; 747_D_11; 811_D_12; 848_C_10; 854_E_10; 870_G_10; from top of Chrl linkage group"
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DNA segment containing
                                                                                                                                                                                                                              Score 10; DB 133;
Pred. No. 2.46e+01;
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 (CA) repeat; clone
                                                                                                                                                                                                                                                                    Length 269;
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                           Dib C., Faure S.,
                                                                                                                                          Submitted (01-SEP-1995) to the EMBL/GenBank/DDBJ databases. Genethon, B.P. 60, 91002 Evry Cedex France. E-mail: Jean.Weissenbach@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Animalia; Metazoa; Chordata; Theria; Eutheria; Primates; Haplorhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFMa244wh5; single read.
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   Millasseau P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microsatellite marker; repeat polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA repeat; dinucleotide repeat; GT repeat; microsatellite
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(Rel. 47, Last updated, Version 3)
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82 A; 79 C; 64 G; 44 T; 3 other;
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/chromosome="1"
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/cell_line="CEPH 134702"
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   , Fizames C.,
arc S., Hazan
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Samson D.,
1 J., Seboun
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Drouot N., Vignal A., E., Lathrop M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Кеy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 380:152-154(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microsatellites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gyapay G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full automatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A comprehensive genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                    Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           н65997
                     Email: est@watson.wustl.edu
High quality sequence stops: 189
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H65997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yr73c10.r1 Homo sapiens cDNA clone 210930
                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                     Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA was primed with a Pac I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and spleen from a 20 week-post conception male fetus. 1st strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                            Washington University School of Medicine
                                                                                                                                                                                    WashU-Merck EST Project
                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                   Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFLS vector=pT7T3D (Pharmacia) with a modified polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human clone=210930 primer=M13RP1 library=Soares fetal liver spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 290)
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                                                                                                                                     Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="cloning vector is M13mp18"
82 A; 79 C; 64 G; 44 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/cell_line="CEPH 134702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        map of the human genome based on 5,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 174;
Pred. No. 2.46e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,,</u>
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                             expression
C.R. Acad. Sci., III, Sci. Vie 318, 263-272 (1995)
Clone library from B.Soares, Psychiatry Dept. Columbia University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z42301
                                             Stretch_removed: nothing Normalization_method: Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Genexpress cDNA program Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygli; Choanata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. sapiens partial
                                                                                                                                                                                 Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5' \rightarrow 3' into the HindIII \rightarrow NotI sites of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                           Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
Sebastiani-Kabaktchis, C. and Tessier, A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Auffray, C., Behar, G., Bois, F., Boucher, C., da Silva, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genethon, B.P. 60, 91002 Evry Cedex France and Genetique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genexpress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            partial cDNA sequence; transcribed sequence fragment
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Genexpress_sequence_idt: y1c-0eh08;
                        Genexpress_library_idt: C;
                                                                                           cDNA sequence colinear to mRNA
                                                                                                               Primer: M13_reverse
                                                                                                                                  Sequencing method: single read,
                                                                                                                                                                                                                                                                                                                                      IMAGE: Integated molecular analysis of the human genome and its
                                                                                                                                                                                                                                                                                                                                                                                                    Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genexpress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 292)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <1..>290
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/clone="210930"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequence; clone c-0eh08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10; DB 26;
Pred. No. 2.46e+01;
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                                                                                                                                        full automatic;
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                                                 P.N.A.S
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Best Local Similarity 100.0%;
Matches 10; Conservative
                               Query Match 100.0%;
Best Local Similarity 100.0%;
         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1996 (Rel. 47, Created)
23-MAR-1996 (Rel. 47, Last updated, Version 3)
H.sapiens (D17S1818) DNA segment containing (CA) repeat; clone AFMa312zc9; single read.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dib C., Faure S., Fizames C., Samson D., Drouot N., Vignal A., Millasseau P., Marc S., Hazan J., Seboun E., Lathrop M., Gyapay G., Morissette J., Weissenbach J.; Gyapay G., Morissette J., Weissenbach J.; "A comprehensive genetic map of the human genome based on 5,264".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-SEP-1995) to the EMBL/GenBank/DDBJ databases. Genethon, B.P. 60, 91002 Evry Cedex France. E-mail: Jean.Meissenbach@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism; STS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSA312ZC9 standard; DNA; STS; 295 BP. 252895;
                                                                                                                                        Sequence 295
                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microsatellites";
Nature 380:152-154(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 aggcatgcct 275
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      10;
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      Conservative
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                                                                                                                                                                                                                                       /organism="Homo sapiens"
/cell_line="CEPH 134702"
/clone_lib="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /isolate="muscular atrophy patient"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="3 months old"
                                                                                                                                     /note="cloning vector is M13mp18" 65 A; 98 C; 45 G; 81 T; 6 other;
                                                                                                                                                                                                       /chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Score 10; DB 174; Length 295; Pred. No. 2.46e+01; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 10; DB 39;
Pred. No. 2.46e+01;
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Db 151 a	aggcatgcct 160
Cp 10 A	AGGATGCCT 1
RESULT 11	
LOCUS DEFINITION	H.sapiens (D17s1818) DNA segment containing (CA) repeat: clone
	2zc9; single read.
ACCESSION NID	
KEYWORDS	CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism; STS.
ORGANISM	Homo sapiens
	yotae; brata;
REFERENCE AUTHORS	to 295)
TITLE	Direct Submission Submitted (01-SED-1995) Comptton B D 60 91000 Evry Codey France
DEFERENCE	h@genethon.fr
AUTHORS	ib,C., Faure,S illasseau,P., orissette,J. a
TITLE	A comprehensive genetic map of the human genome based on $5,264$ microsatellites
JOURNAL COMMENT FEATURES	Nature 380, 152-154 (1996) full automatic. Topation/Onalifiers
source	1.295 /organism="Homo sa /note="cloning vec /cell line="CEPH 1 /clone lib="genomi
BASE COUNT ORIGIN	/ciromosome="17" 65 a 98 c 45 g 81 t 6 others
Query Match Best Local Matches	cch 100.0%; Score 10; DB 136; Length 295; al Similarity 100.0%; Pred. No. 2.46e+01; 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 151 a Cp 10 A	aggcatgcct 160            AGCATGCCT 1
RESULT 12 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE	N46803 309 bp mRNA EST 14-FEB-1996 yy52e05.rl Homo sapiens cDNA clone 277184 5'. N46803 g1187969 EST. human clone=277184 primer=T7 library=Soares multiple sclerosis human clone=277187 (Pharmacia) with a modified polylinker V_TYPE: phagemid host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI 46 year old male. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGCTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTT

through one round of normalization to a Cot = 5. Library

RI sites of a modified pT7T vector (Pharmacia). Library went

Mar 25 02:57

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LOCUS
DEFINITION
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BASE COUNT
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Best Local Similarity 100.0%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 AGGCATGCCT 1
                                                                                                                                                                                                                                                                                            yj85g05.rl Homo sapiens cDNA clone 155576 5 R71722
                  modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis lesions from one patient was kindly provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4
Soares and M.Fatima Bonaldo
                                                                 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a
                                                                                                                                                                   (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsitel=Not I Rsite2=Eco RI Adult female.
                                                                                                                                                                                                                                                                       g845754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Source: IMAGE Consortium, LINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Archonta; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dr. Kevin G.
                                                                                                                    human clone=155576 library=Soares breast 2NbHBst vector=pT7T3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 314 286 1810
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a 66 c
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Pred. No. 2.46e+01;
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Best Local Similarity 100.0%;
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                             Mus musculus (strain C57BL/6Jsub species domesticus, ) decidual tissue (day 6.5-8.5 of gestation) cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                      D18866
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
                                           Shoko Kawamoto
                                                                Submitted (10-Sep-1993) to DDBJ by:
                                                                                      Unpublished (1993)
                                                                                                              cDNA sequencing
                                                                                                                                                         Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.
                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                  EST(expressed sequence tag); Gene signature(GS); development;
                                                                                                                                                                                                                                                                                                                                                                                            g1089499
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Osaka University
                   Institute for Cellular and Molecular Biology
                                                                                                                                    Analysis of gene expression in mouse embryogenesis by 3'-directed
                                                                                                                                                                                                         Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                             transcribed sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                               (bases 1 to 313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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/clone="155576"
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Phone: 06-879-7992 Suita, Osaka, 565

Japan

3-1, Yamadaoka

Fax : 06-877-1922

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BASE COUNT
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                                                                                                                                                                                                                                                                Kelley J.M., Klimek, K.M., Kelley, J.C., Liu, L.-1., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., 'Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST44578 Homo sapiens cDNA 5' end similar to
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                                                                     Unpublished (1995)
                                                                                                                                                                            Based Upon 52 Million Basepairs of cDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-acetylglucosaminyl(beta 1-6) transferase 1 (HT:992). T28441
                                                                                         Contact: Venter, JC
                                                                                                                                                                                                            Initial Assessment of Human Gene Diversity and Expression Patterns
                                                                                                                                                                                                                                               Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human primer=M13 Reverse library=Human Brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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86 c 91 g 62 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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(tdbinfo@tdb.tigr.org) For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database Email: tdbinfo@tdb.tigr.org Fax: 3018699423

Location/Qualifiers

FEATURES source

<1..>313 /organism="Homo sapiens"
/note="human"

mRNA BASE COUNT 64 c 65 g

ORIGIN Query Match 100.0%; Best Local Similarity 100.0%; Pred. No. 2.46e+01 Score 10; 100 t DB 109; Length 313;

В Matches 10; Conservative Mismatches

Indels

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Job time : 62 secs Search completed: Tue Mar 25 02:58:57 1997